```
1                                                  31
TCG ACT ATG AAT GCT GAT ACT GCT CCA ACA TCT CCT TGT CCT TCC ATA TCT TCC CAG AAC
ser thr met asn ala asp thr ala pro thr ser pro cys pro ser ile ser ser gln asn

61                                                 91
TCA AGC TCC TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC AGC ATG TTC GAT CGG ACT TCC
ser ser ser cys ser ser phe gln asp gln lys ile ala ser met phe asp arg thr ser

                                                       Cadherin
121                                                151     |xx EC motif xx|
AGA GTA CCC GCC AGC AGC ACT TCC TCA CCG GGG CTC CTC TTC ACA GAA CTG GCT GCT GCC
arg val pro ala ser ser thr ser ser pro gly leu leu phe thr glu leu ala ala ala

181                                                211
CTG GAT GCC GAA GGG GAA GGA ATC AGC GAA GTA CAA AGG AAA GCT GTC AGT GCA ATT CAC
leu asp ala glu gly glu gly ile ser glu val gln arg lys ala val ser ala ile his

241                                                271
AGC CTG CTA AGT TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA CCA GAG GTG AAG GTC AAA
ser leu leu ser ser his asp leu asp pro arg cys val lys pro glu val lys val lys

301                                                331
ATC GCC GCC CTT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT GCT TTG CCA CAG CTC TGT
ile ala ala leu tyr leu pro leu val gly ile ile leu asp ala leu pro gln leu cys

361                                                391
GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC TCG GAT GAA GAA CAA GAA
asp phe thr val ala asp thr arg arg tyr arg thr ser gly ser asp glu glu gln glu

421                                                451
GGA GCC GGT GCC ATT ACC CAG AAT GTG GCT CTG GCC ATA GCA GGG AAT AAT TTC AAT TTG
gly ala gly ala ile thr gln asn val ala leu ala ile ala gly asn asn phe asn leu

481                                                511
AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG TAC AAC ATG CTG AAC GCG
lys thr ser gly ile val leu ser ser leu pro tyr lys gln tyr asn met leu asn ala

541                                                571
GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG AAA AAT GCT GAT CAG AGC
asp thr thr arg asn leu met ile cys phe leu trp ile met lys asn ala asp gln ser

601                                                631
CTC ATT AGG AAG TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC AAC AGG ATT TTA GAT CTA
leu ile arg lys trp ile ala asp leu pro ser thr gln leu asn arg ile leu asp leu
```

FIG. 1
1 of 6

661 691
CTT TTC ATC TGT GTG TTA TGT TTT GAG TAT AAG GGA AAA CAG AGT TCT GAC AAA GTC AGT
leu phe ile cys val leu cys phe glu tyr lys gly lys gln ser ser asp lys val ser

721 751
ACC CAA GTC CTG CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG GAA GAG GCT TTG CTG CGT
thr gln val leu gln lys ser arg asp val lys ala arg leu glu glu ala leu leu arg

781 811
GGG GAA GGG GCC AGA GGG GAG ATG ATG CGC CGC CGG GCT CCA GGG AAC GAC CGA TTT CCA
gly glu gly ala arg gly glu met met arg arg arg ala pro gly asn asp arg phe pro

841 871
GGC CTA AAT GAA AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT TGG CGG CAA GCT AAT GAG
gly leu asn glu asn leu arg trp lys lys glu gln thr his trp arg gln ala asn glu

901 931
AAG CTA GAT AAA ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG ATC AGT GGC AAT CTG GCT
lys leu asp lys thr lys ala glu leu asp gln glu ala leu ile ser gly asn leu ala

961 991
ACA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT ATC CAG GCG AGC TCG GCT
thr glu ala his leu ile ile leu asp met gln glu asn ile ile gln ala ser ser ala

1021 1051
CTG GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG CTG GTG AAT TCT CTG AAC
leu asp cys lys asp ser leu leu gly gly val leu arg val leu val asn ser leu asn

1081 1111
TGT GAT CAG AGT ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA CTC CGT GCT CTC ATC GCC
cys asp gln ser thr thr tyr leu thr his cys phe ala thr leu arg ala leu ile ala

1141 1171
AAG TTT GGA GAC TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT TTC GAC CTA TGT CAC CAA
lys phe gly asp leu leu phe glu glu glu val glu gln cys phe asp leu cys his gln

1201 1231
GTC CTG CAC CAC TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC CAA GCC TGT GCC ACC CTT
val leu his his cys ser ser ser met asp val thr arg ser gln ala cys ala thr leu

1261 1291
TAC CTC CTC ATG AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT GCA AGA GTA AAG ATG CAA
tyr leu leu met arg phe ser phe gly ala thr ser asn phe ala arg val lys met gln

1321 1351
GTA ACC ATG TCC CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC TTT AAT GAA GAG CAC CTG
val thr met ser leu ala ser leu val gly arg ala pro asp phe asn glu glu his leu

1381 1411
AGA AGA TCC TTG AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC ACA GCC ATG CAG ATG ACT
arg arg ser leu arg thr ile leu ala tyr ser glu glu asp thr ala met gln met thr

1441 1471
CCT TTT CCC ACC CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT AGC ATC TTA TAT GAC ACA
pro phe pro thr gln val glu glu leu leu cys asn leu asn ser ile leu tyr asp thr

1501 1531
GTG AAA ATG AGG GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG GAT CTC ATG TAC AGA ATT
val lys met arg glu phe gln glu asp pro glu met leu met asp leu met tyr arg ile

1561 1591
GCC AAG AGT TAC CAG GCA TCT CCT GAT CTG CGG CTG ACC TGG CTC CAG AAC ATG GCA GAG
ala lys ser tyr gln ala ser pro asp leu arg leu thr trp leu gln asn met ala glu

1621 |xxxxxxxxxxxxxxxxxxxxxx transmembrane domain xxxxxxx
AAA CAC ACC AAG AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC CTG GTG CAC GCC GCT GCG
lys his thr lys lys lys cys tyr thr glu ala ala met cys leu val his ala ala ala

xxxxxxxxxxxxxxxxxxxxxxx| 1711
TTA GTG GCT GAG TAT CTG AGC ATG CTG GAG GAC CAC AGC TAC CTG CCC GTG GGC AGT GTC
leu val ala glu tyr leu ser met leu glu asp his ser tyr leu pro val gly ser val

1741 1771
AGC TTC CAG AAT ATT TCT TCC AAT GTG CTG GAG GAG TCT GTG GTC TCT GAG GAC ACC CTG
ser phe gln asn ile ser ser asn val leu glu glu ser val val ser glu asp thr leu

1801 1831
TCA CCT GAC GAG GAT GGG GTG TGC GCA GGC CAG TAC TTC ACC GAG AGT GGC CTG GTA GGC
ser pro asp glu asp gly val cys ala gly gln tyr phe thr glu ser gly leu val gly

1861 1891
CTC CTG GAG CAG GCC GCG GAG CTC TTC AGC ACG GGA GGC TTA TAT GAG ACA GTT AAT GAG
leu leu glu gln ala ala glu leu phe ser thr gly gly leu tyr glu thr val asn glu

1921 1951
GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA TTC CGG AAG CTG ACA CTC
val tyr lys leu val ile pro ile leu glu ala his arg glu phe arg lys leu thr leu

1981 2011
ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC AAG GAT CAT AAG AGA ATG
thr his ser lys leu gln arg ala phe asp ser ile val asn lys asp his lys arg met

2041 |xxxxx ITAM xxxx| 2071
TTT GGA ACC TAC TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT GGG GAT TTG GAT GAA CAG
phe gly thr tyr phe arg val gly phe phe gly ser lys phe gly asp leu asp glu gln

```
2101                                                2131
GAG TTT GTC TAC AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG ATC TCA CAT AGA CTA GAG
glu phe val tyr lys glu pro ala ile thr lys leu pro glu ile ser his arg leu glu

2161                                                2191
GCA TTT TAT GGT CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG ATT AAA GAC TCC ACT CCT
ala phe tyr gly gln cys phe gly ala glu phe val glu val ile lys asp ser thr pro

2221                                                2251
GTG GAC AAA ACC AAG TTG GAT CCT AAC AAG GCC TAC ATA CAG ATC ACT TTT GTG GAG CCC
val asp lys thr lys leu asp pro asn lys ala tyr ile gln ile thr phe val glu pro

2281                                                2311
TAC TTT GAT GAG TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT GAG AAG AAT TTC AAC CTC
tyr phe asp glu tyr glu met lys asp arg val thr tyr phe glu lys asn phe asn leu

2341                                                2371
CGG AGG TTC ATG TAC ACC ACC CCG TTC ACC CTG GAG GGG CGG CCT CGG GGA GAG CTG CAT
arg arg phe met tyr thr thr pro phe thr leu glu gly arg pro arg gly glu leu his

2401                                                2431
GAG CAG TAC AGA AGG AAC ACA GTC CTG ACC ACT ATG CAC GCC TTC CCC TAC ATC AAG ACC
glu gln tyr arg arg asn thr val leu thr thr met his ala phe pro tyr ile lys thr

2461                                                2491                |xxxxxxxxxxxxxxxxxxxxxxx
AGG ATC AGC GTC ATC CAG AAG GAG GAG TTT GTT TTG ACA CCG ATT GAA GTT GCC ATT GAA
arg ile ser val ile gln lys glu glu phe val leu thr pro ile glu val ala ile glu

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coiled coil 1 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
GAC ATG AAG AAG AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC CAG GAG CCG CCT GAT GCA
asp met lys lys lys thr leu gln leu ala val ala ile asn gln glu pro pro asp ala

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx|    2611
AAG ATG CTT CAG ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT GTA AAT CAG GGA CCA CTG
lys met leu gln met val leu gln gly ser val gly ala thr val asn gln gly pro leu

2641                                                2671
GAA GTA GCC CAA GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA AAA CTC TAT CGA CAT CAC
glu val ala gln val phe leu ala glu ile pro ala asp pro lys leu tyr arg his his

2701                                                2731                        |xxxxxxxxxxx
AAC AAG TTG AGG TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT GGT GAA GCT GTA GAG AAA
asn lys leu arg leu cys phe lys glu phe ile met arg cys gly glu ala val glu lys

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coiled coil 2 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
AAC AAG CGT CTC ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG GAA CTC AAA AAG AAC TAT
asn lys arg leu ile thr ala asp gln arg glu tyr gln gln glu leu lys lys asn tyr
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xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx|

AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA ATT CCA GAA CTG TAC AAG
asn lys leu lys glu asn leu arg pro met ile glu arg lys ile pro glu leu tyr lys

2881 2911
CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC AGA TCT AGT TTC AGG AAA
pro ile phe arg val glu ser gln lys arg asp ser phe his arg ser ser phe arg lys

2941 2971
TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA GAA AAG CCA TCT TCA TTC GTG GAG ACT GTG
cys glu thr gln leu ser gln gly ser OCH glu lys pro ser ser phe val glu thr val

3001 3031
GCC CTG CAA CCC TGG AGA AGG ACT TGC TGG TAC TTA AAA AAT GGG ACA TTT GCC ACC CAG
ala leu gln pro trp arg arg thr cys trp tyr leu lys asn gly thr phe ala thr gln

3061 3091
GAC TGA CTG TAC ACT CCC TGA TCA GCC AGC ACT CTG GAA GCT TTG GGA TCC CAG GAA CCA
asp STP

3121 3151
TGG AAT TAT TCC CAA ATG GAC TCT GAC CAG ATT TTT GCC ATA CTG GGG GGT GGC GGG ATG

3181 3211
GAG GAT GGG TAC TCA GGC ATG ACT GCG TAT TTA TTA AAG TGT GTT TTT CCA CAA TGT ACC

3241 3271
AAA CAA GGC ATA AGC AGC TTC TCC TGC TGA CTG GCC AAT CAC TGC CCA TCT GAG AGA TGA

3301 3331
TTT CCT CTG GCC CAT ATT TGA ATT TAT TGG AGT AAC TCA AAT TGC CTG AGG AAA AAT GGA

3361 3391
AAA ATT ATC CAC CAG TCG ATT CAA ACT GAA TTT CAC TCT TTA TAG GAA GGC AGG GCA AAC

3421 3451
TTG TAG GAG TAC GAA ACA TTT TCA ATA AAT CTA CAA AGG GAA GCC TTA CTA CAA TTC CAA

3481 3511
AAA TCA TCA TGG TTG GAA ATT TGG GAG GAG ATT ATT TGT GAA CTT GTT ACC CTT TTG GTA

3541 3571
ATG GTG GAC TAA TTG CTG TAT AGT TAT TTT TGT TTT ATT ATT ACT GTT ACA TTA ATT TAA

3601 3631
CAT GCA TTT ATA GAA GAA TAC ATT CAA AGC ACT GAT GTA GGA GAT ACA CGG TAC TTG GAG

3661 3691
CAG TCA GCC AAA AAT CAC AGA TAC TGC TTT CAC TTA AAT GGA AAC AAT TCT CCG ATA ATG

3721 3751
CTT TGC TTT TTT TCT TAT GTC ACT CTT GTG TAC TAT CTA TTT TTC TCC TCT CTG GGA CCA

3781 3811
AGT TTC TTT TTA TAA AGC AAT AAT ATC TCT GTT TTC ATT TCA GAA CAT TGT GCT GTC TGT

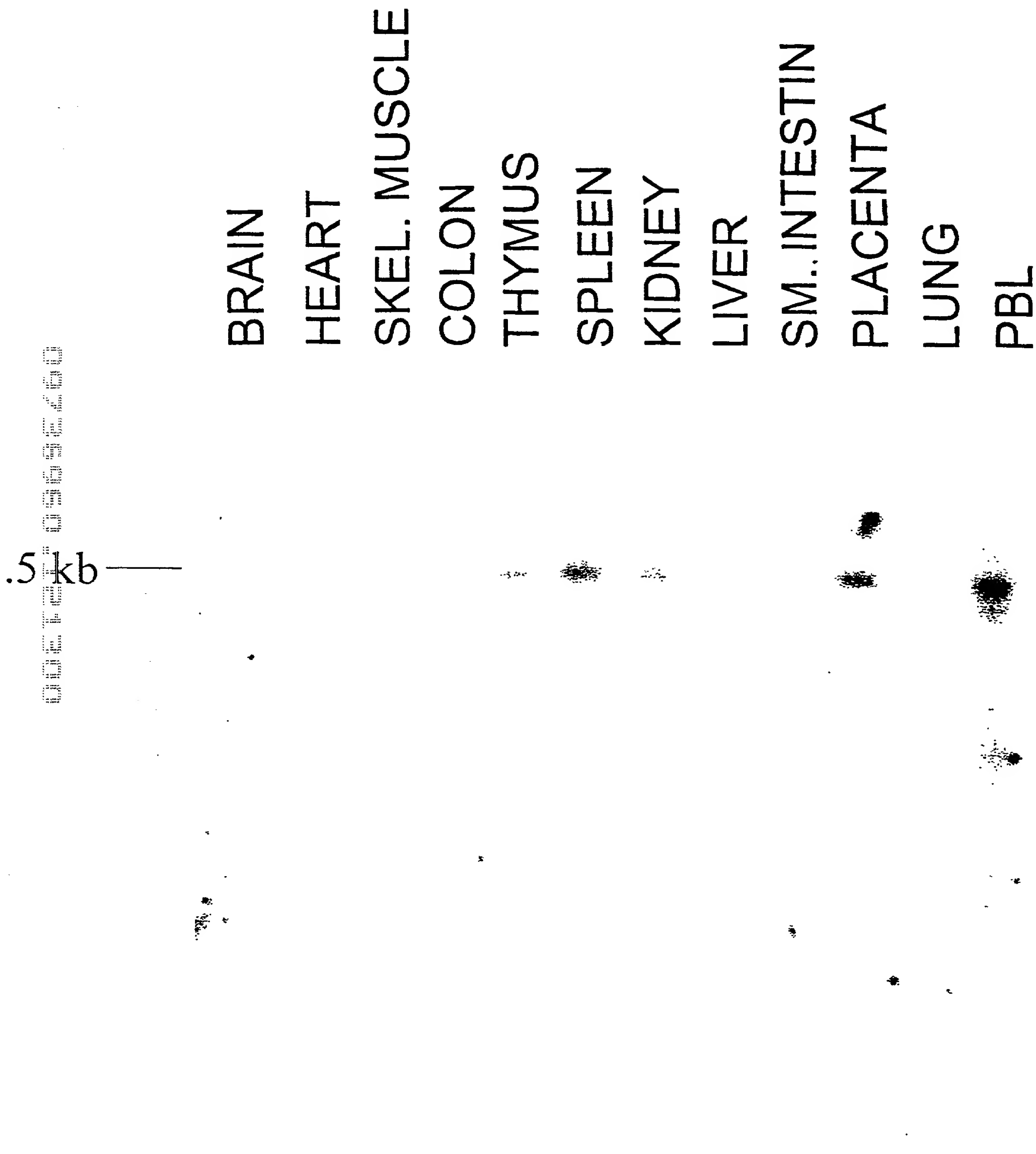
3841 3871
CAG CAT ATG TAT ATC AGC TAC AAA ATA TAT TCA ACT TTG ACT TCT TTT GAC AAA GGA CTT

3901 3931
TAG GAA AAG GAG GAA CAA AGA CAT TAT TTG AGA ATT AAA TTA TAT ATT TTT AAT ATG ACT

3961 3991
GTG ACC TTG ACT GAT AAT AAA GAT GTA ATA AGA ATT GCA AGC TAA AAA AAA AAA AAA AAA

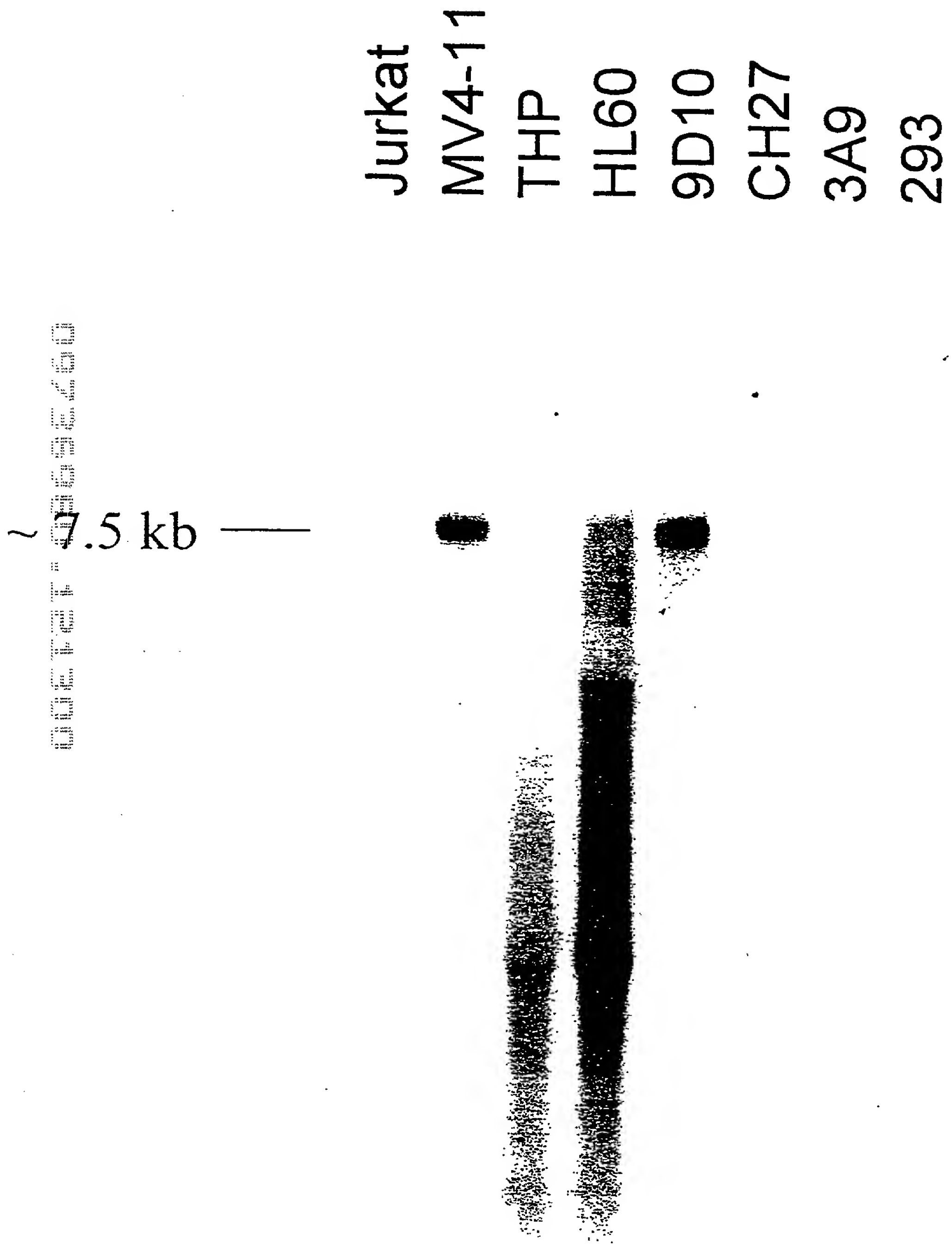
4021
AAC TCG

FIG. 1


BRAIN
HEART
SKEL. MUSCLE
COLON
THYMUS
SPLEEN
KIDNEY
LIVER
SM..INTESTIN
PLACENTA
LUNG
PBL
.5 kb

A

FIG. 2



B

FIG. 2

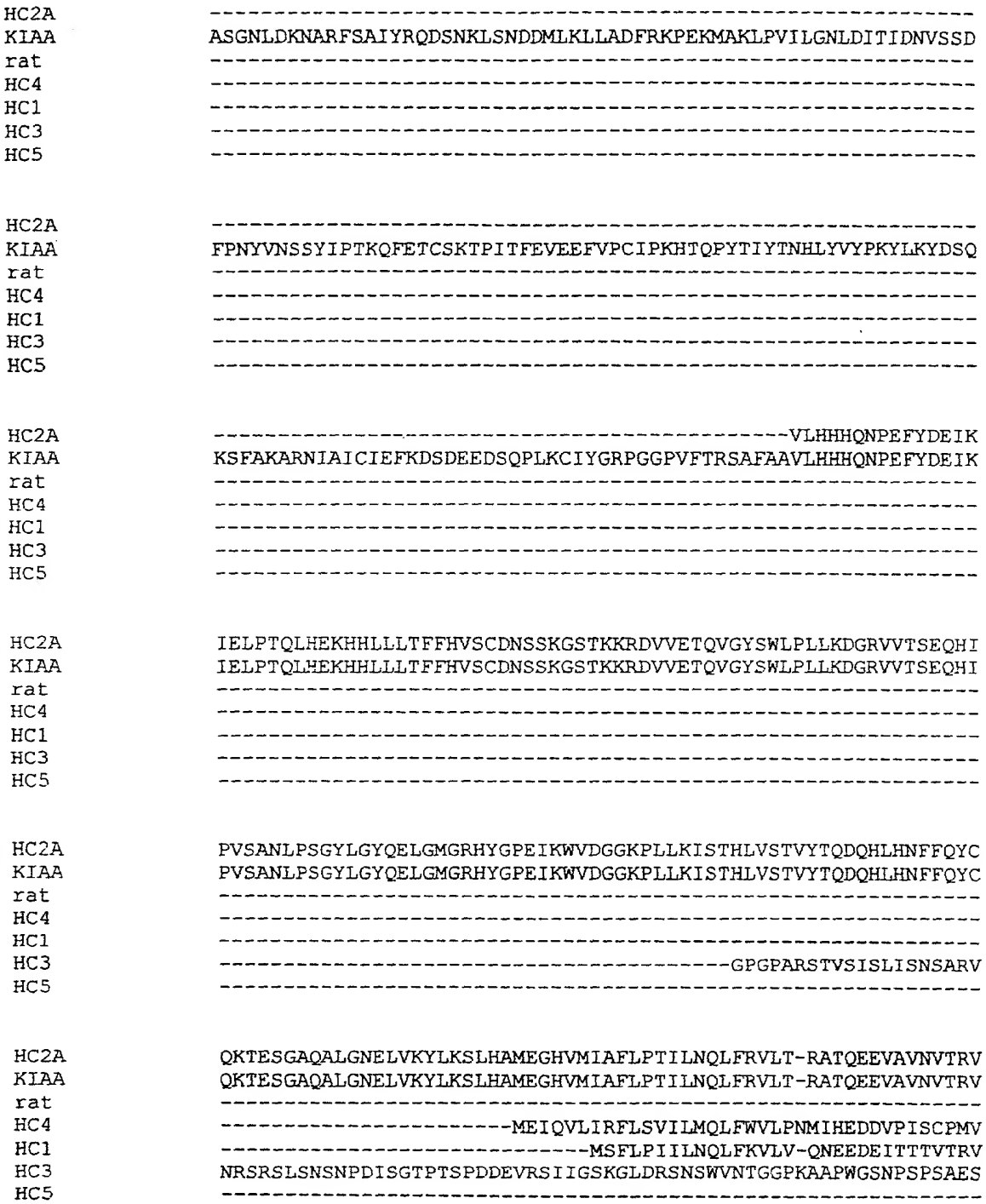

HC2A
KIAA
rat
HC4
HC1
HC3
HC5
ASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPEFYDEIK
IELPTQLHEKHHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
GPGPARSTVSISLISNSARV
QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES

FIG. 3
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A

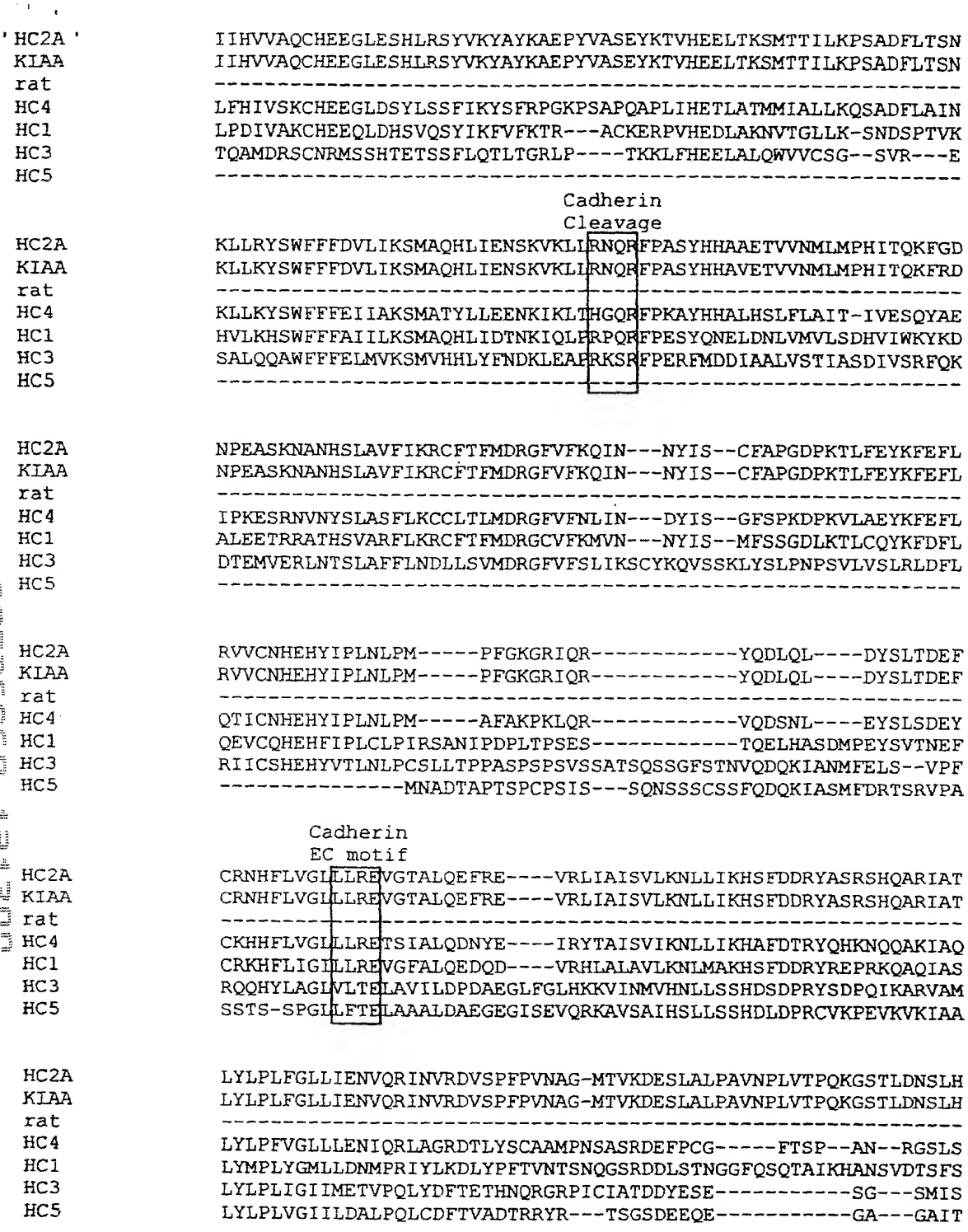
HC2A IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
KIAA IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
rat
HC4 LFHIVSKCHEEGLDSYLSSFIKYSFRPGKPSAPQAPLIHETLATMMIALLKQSADFLAIN
HC1 LPDIVAKCHEEQLDHSVQSYIKFVFKTR---ACKERPVHEDLAKNVTGLLK-SNDSPTVK
HC3 TQAMDRSCNRMSSHTETSSFLQTLTGRLP----TKKLFHEELALQWVVCSG--SVR---E
HC5
Cadherin
Cleavage
HC2A KLLRYSWFFFDVLIKSMAQHLIENSKVKLLRNQRFPASYHHAAETVVNMLMPHITQKFGD
KIAA KLLKYSWFFFDVLIKSMAQHLIENSKVKLLRNQRFPASYHHAVETVVNMLMPHITQKFRD
rat
HC4 KLLKYSWFFFEIIAKSMATYLLEENKIKLTHGQRFPKAYHHALHSLFLAIT-IVESQYAE
HC1 HVLKHSWFFFAIILKSMAQHLIDTNKIQLPRPQRFPESYQNELDNLVMVLSDHVIWKYKD
HC3 SALQQAWFFFELMVKSMVHHLYFNDKLEAPRKSRFPERFMDDIAALVSTIASDIVSRFQK
HC5
HC2A NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
KIAA NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
rat
HC4 IPKESRNVNYSLASFLKCCLTLMDRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL
HC1 ALEETRRATHSVARFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTLCQYKFDFL
HC3 DTEMVERLNTSLAFFLNDLLSVMDRGFVFSLIKSCYKQVSSKLYSLPNPSVLVSLRLDFL
HC5
HC2A RVVCNHEHYIPLNLPM-----PFGKGRIQR----------YQDLQL----DYSLTDEF
KIAA RVVCNHEHYIPLNLPM-----PFGKGRIQR----------YQDLQL----DYSLTDEF
rat
HC4 QTICNHEHYIPLNLPM-----AFAKPKLQR----------VQDSNL----EYSLSDEY
HC1 QEVCQHEHFIPLCLPIRSANIPDPLTPSES----------TQELHASDMPEYSVTNEF
HC3 RIICSHEHYVTLNLPCSLLTPPASPSPSVSSATSQSSGFSTNVQDQKIANMFELS--VPF
HC5 ----------MNADTAPTSPCPSIS---SQNSSSCSSFQDQKIASMFDRTSRVPA
Cadherin
EC motif
HC2A CRNHFLVGLLLREVGTALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
KIAA CRNHFLVGLLLREVGTALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
rat
HC4 CKHHFLVGLLLRETSIALQDNYE----IRYTAISVIKNLLIKHAFDTRYQHKNQQAKIAQ
HC1 CRKHFLIGLLLREVGFALQEDQD----VRHLALAVLKNLMAKHSFDDRYREPRKQAQIAS
HC3 RQQHYLAGLVLTELAVILDPDAEGLFGLHKKVINMVHNLLSSHDSDPRYSDPQIKARVAM
HC5 SSTS-SPGLLFTELAAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPRCVKPEVKVKIAA
HC2A LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
KIAA LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
rat
HC4 LYLPFVGLLLENIQRLAGRDTLYSCAAMPNSASRDEFPCG-----FTSP--AN--RGSLS
HC1 LYMPLYGMLLDNMPRIYLKDLYPFTVNTSNQGSRDDLSTNGGFQSQTAIKHANSVDTSFS
HC3 LYLPLIGIIMETVPQLYDFTETHNQRGRPICIATDDYESE----------SG---SMIS
HC5 LYLPLVGIILDALPQLCDFTVADTRRYR---TSGSDEEQE----------GA---GAIT

FIG. 3
2 of 5

A

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HC2A        KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSS
KIAA        KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSS
rat         ------------------------------------------------------------
HC4         TDKDTAYGSFQNG--------HGIKREDSRGSLIP-EGATGFPDQGNTGEN-----TRQS
HC1         KDVLNSIAAFSS------IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL
HC3         QTVAMAIAGTSVPQ-------------------LTRPGSFLLTSTSGRQHT---------
HC5         QNVALAIAGNNFN--------------------LKTSG-IVLSSLPYKQYN---------

HC2A        TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL
KIAA        TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL
rat         ------------------------------------------------------------
HC4         STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISEDTLLTYWN-KVSPQELINILILLEVCL
HC1         ALIGSTLRFDRLDQAETRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSILDVCL
HC3         ----------TFSAESSRSLLICLLWVLKN-ADETVLQKWFTDLSVLQLNRLLDLLYLCV
HC5         ----------MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV

HC2A        HQFQYMGKRYIARNQEGLG--PIVHDRKS-----------------QTLPVSRNRTGMM
KIAA        HQFQYMGKRYIAR----------------------------------------TGMM
rat         ------------------------------------------------------------
HC4         FHFRYMGKRNIARVHDAWLSKHFGIDRKS-----------------QTMPALRNRSGVM
HC1         QNFRYLGKRNIIRKIAAAF--KFVQSTQNNGTLKGSNPSCQTSGLLAQWMHSTSRHEGHK
HC3         SCFEYKGKKVFERMNSLTFK--KSKDMRAK--------------LEEAILGSIGARQEMV
HC5         LCFEYKGKQSSDKVSTQVLQ--KSRDVKAR--------------LEEALLRGEGARGEMM

HC2A        HARLQQL---------GSLDNS---------LTFNHSYGHSDADVLHQSLLEANIATEVC
KIAA        HARLQQL---------GSLDNS---------LTFNHSYGHSDADVLHQSLLEANIATEVC
rat         ------------------------------------------------------------
HC4         QARLQHL---------SSLESS---------FTLNHSSTTTEADIFHQALLEGNTATEVS
HC1         QHRSQTLPIIRGK---NALSNPKL----LQMLDNTMTSNSNEIDIVHHVDTEANIATEGC
HC3         RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNTEKLDKSRAEIEHEALIDGNLATEAN
HC5         RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH

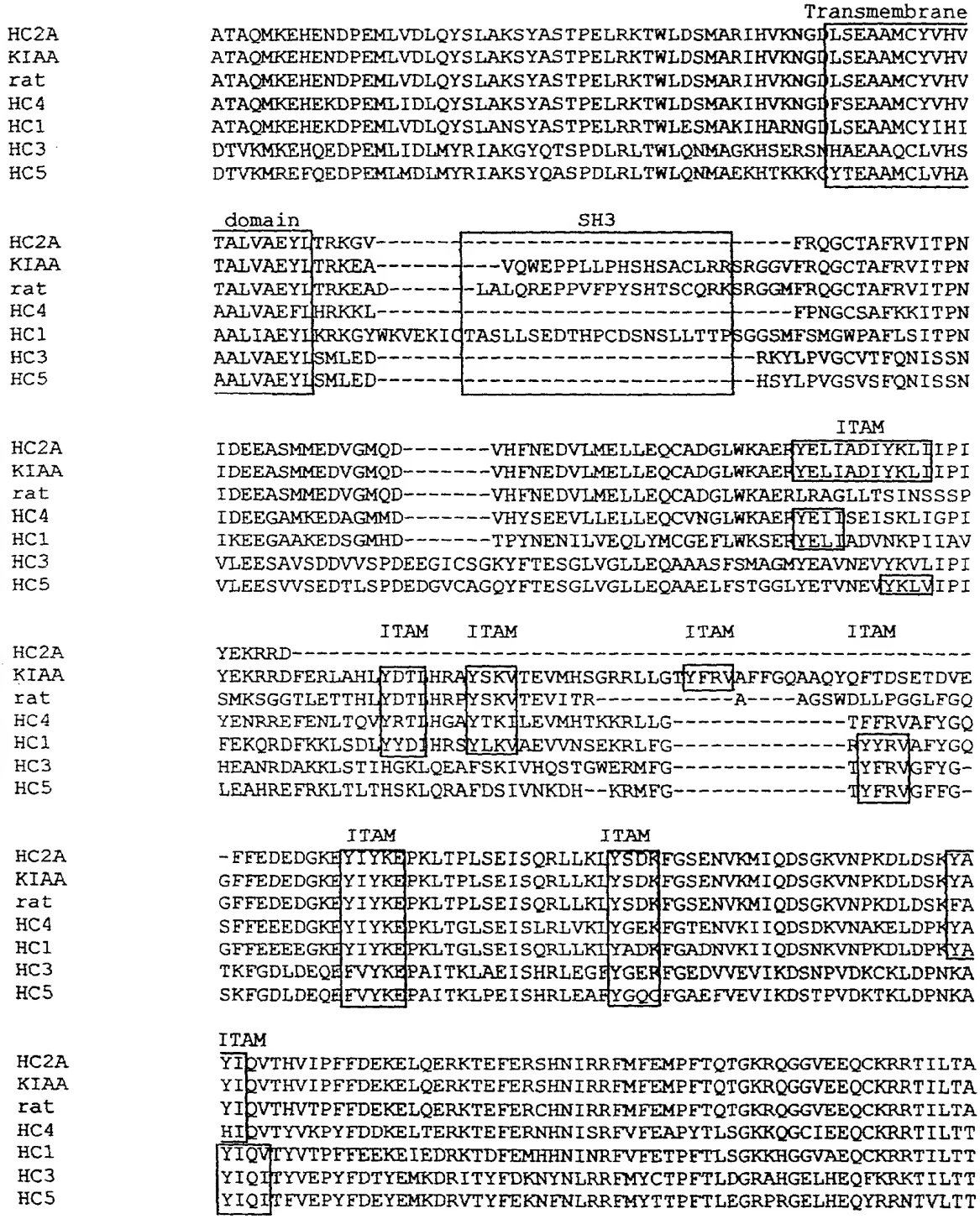
HC2A        LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
KIAA        LTALDTLSLFTLAFKNQLLADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
rat         ------------------KLSRGHSPLMKKVFDVYLCFLQKHQSEMALKNVFTALRSLIY
HC4         LTVLDTISFFTQCFKTHFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS
HC1         LTILDLVSLFTQTHQRQLQQCDCQNSLMKRGFDTYMLFFQVNQSATALKHVFASLRLFVC
HC3         LIILDTLEIVVQTVS--VTES--KESILGGVLKVLLHSMACNQSAVYLQHCFATQRALVS
HC5         LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNCDQSTTYLTHCFATLRALIA

HC2A        KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
KIAA        KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
rat         KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTH
HC4         KFPSAFFKGRVNMCAAFCYEVLKCCTSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTH
HC1         KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH
HC3         KFPELLFEEETEQCADLCLRLLRHCSSSIGTIRSHPSASLYLLMRQNFEIGN--NFARVK
HC5         KFGDLLFEEEVEQCFDLCHQVLHHCSSSMDVTRSQACATLYLLMRFSFGATS--NFARVK

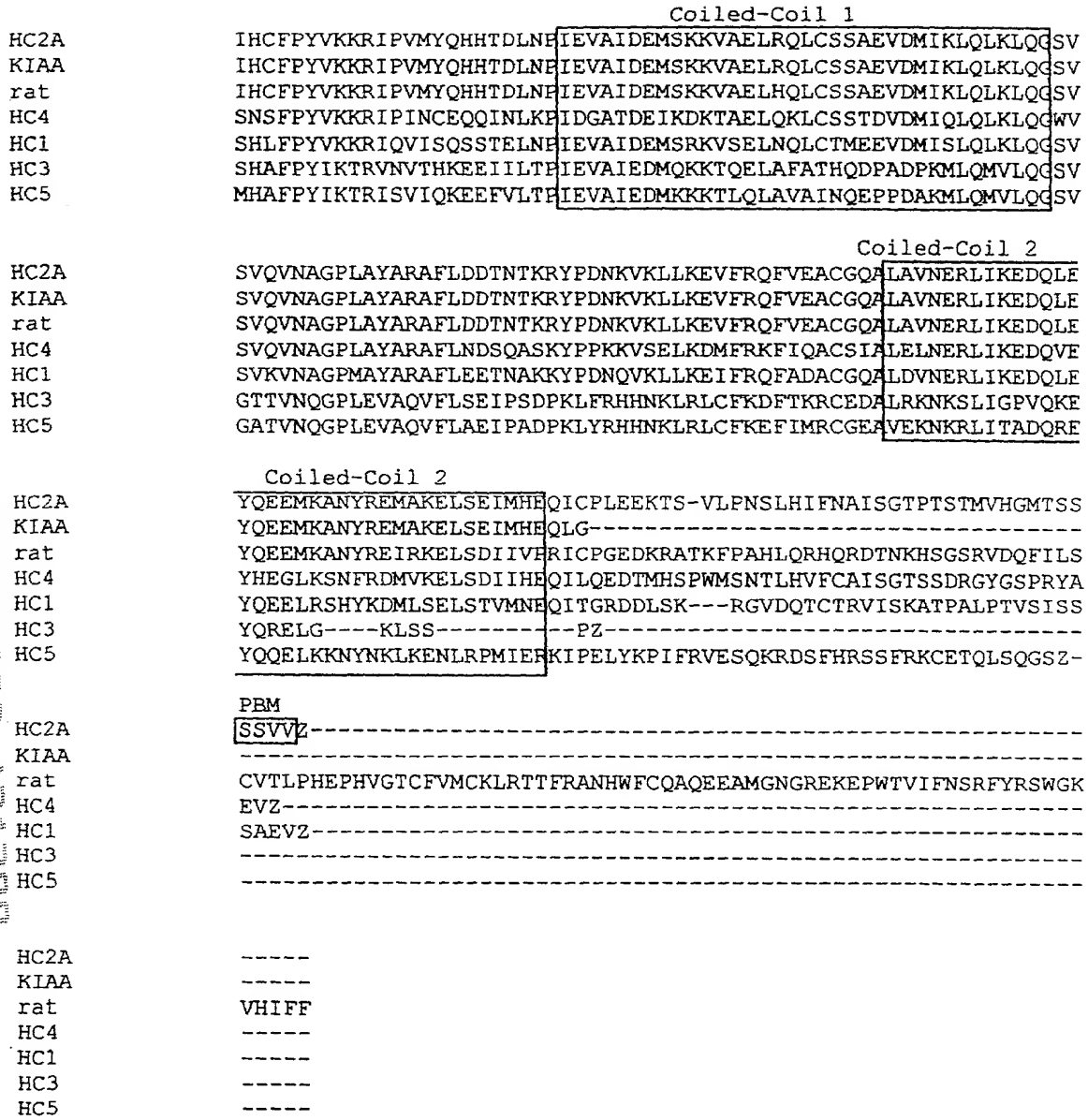
HC2A        LQVIISVSQLIADVVGIGETRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLM
KIAA        LQVIISVSQLIADVVGIGGTRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLM
rat         LQVIISLSQLIADVVGIGGTRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLM
HC4         LQIIIAVSQLIADVALSGGSRFQESLFIINNFANSDRPMLARAFPAEVKDLTKRIRTVLM
HC1         LQLIKAVSQLIAD-AGIGGSRFQHSLAITNNFANGDKQMKNSNFPAEVKDLTKRIRTVLM
HC3         MQVPMSLSSLVGTSQNFNEEFLRRSLKTILTYAEEDLELRETTFPDQVQDLVFNLHMILS
HC5         MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMTPFPTQVEELLCNLNSILY
```

A

FIG. 3
3 of 5

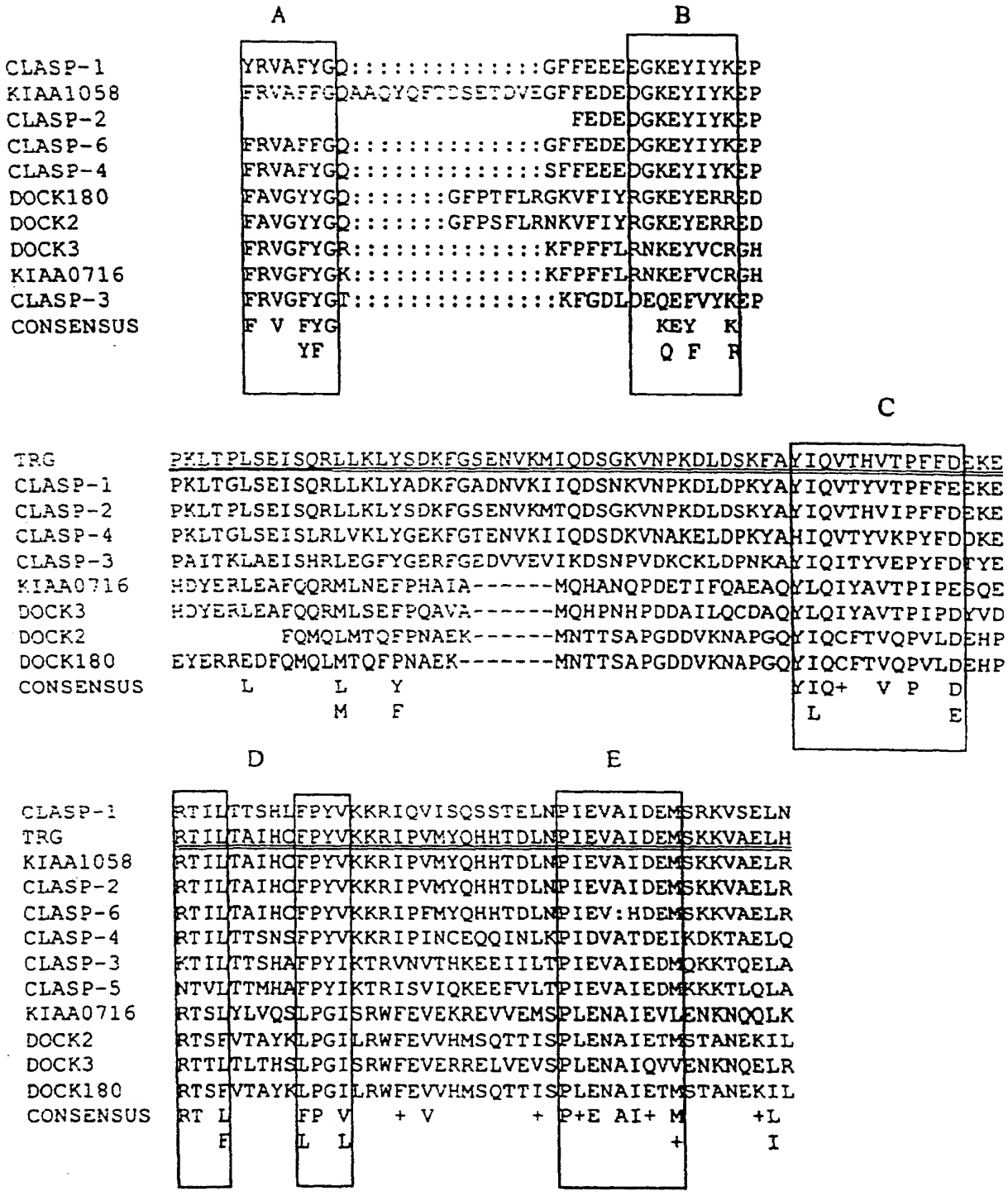

Transmembrane
HC2A ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHV
KIAA ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHV
rat ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHV
HC4 ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLDSMAKIHVKNGDFSEAAMCYVHV
HC1 ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLESMAKIHARNGDLSEAAMCYIHI
HC3 DTVKMKEHQEDPEMLIDLMYRIAKGYQTSPDLRLTWLQNMAGKHSERSNHAEAAQCLVHS
HC5 DTVKMREFQEDPEMLMDLMYRIAKSYQASPDLRLTWLQNMAEKHTKKKQYTEAAMCLVHA
domain
SH3
HC2A TALVAEYLTRKGV----------FRQGCTAFRVITPN
KIAA TALVAEYLTRKEA----------VQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRVITPN
rat TALVAEYLTRKEAD----------LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4 AALVAEFLHRKKL----------FPNGCSAFKKITPN
HC1 AALIAEYLKRKGYWKVEKICTASLLSEDTHPCDSNSLLTTPSGGSMFSMGWPAFLSITPN
HC3 AALVAEYLSMLED----------RKYLPVGCVTFQNISSN
HC5 AALVAEYLSMLED----------HSYLPVGSVSFQNISSN
ITAM
HC2A IDEEASMMEDVGMQD-------VHFNEDVLMELLEQCADGLWKAEHYELIADIYKLIIPI
KIAA IDEEASMMEDVGMQD-------VHFNEDVLMELLEQCADGLWKAEHYELIADIYKLIIPI
rat IDEEASMMEDVGMQD-------VHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSSP
HC4 IDEEGAMKEDAGMMD-------VHYSEEVLLELLEQCVNGLWKAEHYEIISEISKLIGPI
HC1 IKEEGAAKEDSGMHD-------TPYNENILVEQLYMCGEFLWKSERYELIADVNKPIIAV
HC3 VLEESAVSDDVVSPDEEGICSGKYFTESGLVGLLEQAAASFSMAGMYEAVNEVYKVLIPI
HC5 VLEESVVSEDTLSPDEDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKLVIPI
ITAM ITAM ITAM ITAM
HC2A YEKRRD----------
KIAA YEKRRDFERLAHLYDTLHRAYSKVTEVMHSGRRLLGTYFRVAFFGQAAQYQFTDSETDVE
rat SMKSGGTLETTHLYDTLHRPYSKVTEVITR----------A----AGSWDLLPGGLFGQ
HC4 YENRREFENLTQVYRTLHGAYTKILEVMHTKKRLLG----------TFFRVAFYGQ
HC1 FEKQRDFKKLSDLYYDIHRSYLKVAEVVNSEKRLFG----------RYYRVAFYGQ
HC3 HEANRDAKKLSTIHGKLQEAFSKIVHQSTGWERMFG----------TYFRVGFYG-
HC5 LEAHREFRKLTLTHSKLQRAFDSIVNKDH--KRMFG----------TYFRVGFFG-
ITAM ITAM
HC2A -FFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDRFGSENVKMIQDSGKVNPKDLDSKYA
KIAA GFFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA
rat GFFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKFA
HC4 SFFEEEDGKEYIYKEPKLTGLSEISLRLVKIYGEKFGTENVKIIQDSDKVNAKELDPKYA
HC1 GFFEEEEGKEYIYKEPKLTGLSEISQRLLKIYADKFGADNVKIIQDSNKVNPKDLDPKYA
HC3 TKFGDLDEQEFVYKEPAITKLAEISHRLEGFYGERFGEDVVEVIKDSNPVDKCKLDPNKA
HC5 SKFGDLDEQEFVYKEPAITKLPEISHRLEAFYGQGFGAEFVEVIKDSTPVDKTKLDPNKA
ITAM
HC2A YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
KIAA YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
rat YIQVTHVTPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
HC4 HIQVTYVKPYFDDKELTERKTEFERNHNISRFVFEAPYTLSGKKQGCIEEQCKRRTILTT
HC1 YIQVTYVTPFFEEKEIEDRKTDFEMHHNINRFVFETPFTLSGKKHGGVAEQCKRRTILTT
HC3 YIQITYVEPYFDTYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAHGELHEQFKRKTILTT
HC5 YIQITFVEPYFDEYEMKDRVTYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLTT

A


Coiled-Coil 1
HC2A IHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
KIAA IHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
rat IHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELHQLCSSAEVDMIKLQLKLQGSV
HC4 SNSFPYVKKRIPINCEQQINLKPIDGATDEIKDKTAELQKLCSSTDVDMIQLQLKLQGWV
HC1 SHLFPYVKKRIQVISQSSTELNPIEVAIDEMSRKVSELNQLCTMEEVDMISLQLKLQGSV
HC3 SHAFPYIKTRVNVTHKEEIILTPIEVAIEDMQKKTQELAFATHQDPADPKMLQMVLQGSV
HC5 MHAFPYIKTRISVIQKEEFVLTPIEVAIEDMKKKTLQLAVAINQEPPDAKMLQMVLQGSV
Coiled-Coil 2
HC2A SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
KIAA SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
rat SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
HC4 SVQVNAGPLAYARAFLNDSQASKYPPKKVSELKDMFRKFIQACSIALELNERLIKEDQVE
HC1 SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQALDVNERLIKEDQLE
HC3 GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDALRKNKSLIGPVQKE
HC5 GATVNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEAVEKNKRLITADQRE
Coiled-Coil 2
HC2A YQEEMKANYREMAKELSEIMHEQICPLEEKTS-VLPNSLHIFNAISGTPTSTMVHGMTSS
KIAA YQEEMKANYREMAKELSEIMHEQLG----------
rat YQEEMKANYREIRKELSDIIVERICPGEDKRATKFPAHLQRHQRDTNKHSGSRVDQFILS
HC4 YHEGLKSNFRDMVKELSDIIHEQILQEDTMHSPWMSNTLHVFCAISGTSSDRGYGSPRYA
HC1 YQEELRSHYKDMLSELSTVMNEQITGRDDLSK---RGVDQTCTRVISKATPALPTVSISS
HC3 YQRELG----KLSS---------PZ----------
HC5 YQQELKKNYNKLKENLRPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGSZ-
PBM
HC2A SSVVZ----------
KIAA ----------
rat CVTLPHEPHVGTCFVMCKLRTTFRANHWFCQAQEEAMGNGREKEPWTVIFNSRFYRSWGK
HC4 EVZ----------
HC1 SAEVZ----------
HC3 ----------
HC5 ----------
HC2A -----
KIAA -----
rat VHIFF
HC4 -----
HC1 -----
HC3 -----
HC5 -----

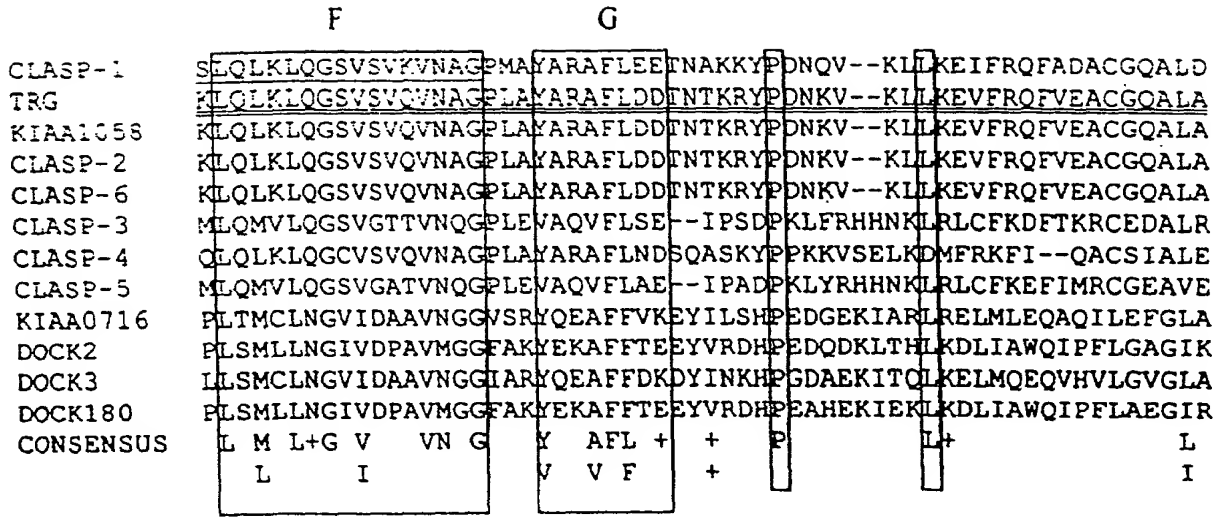
A

FIG. 3
5 of 5


A
B
C
D
E
CLASP-1
KIAA1058
CLASP-2
CLASP-6
CLASP-4
DOCK180
DOCK2
DOCK3
KIAA0716
CLASP-3
CONSENSUS
TRG
CLASP-5

B

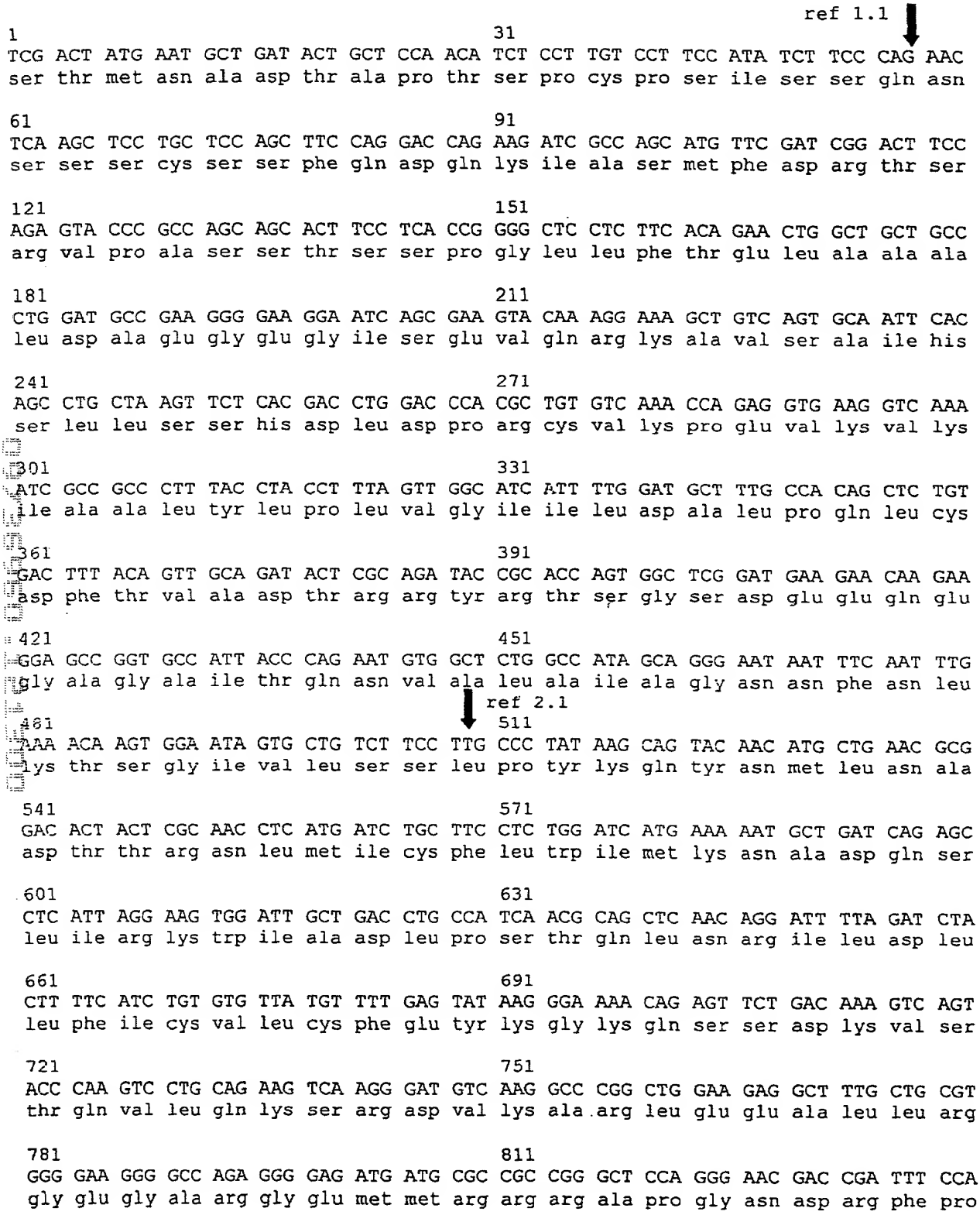
FIG. 3
1 of 2



DOCK1=KIAA0209
DOCK3=KIAA0299
CLASP1variant=KIAA1056

B

FIG. 3
2 of 2


ref 1.1
1
31
TCG ACT ATG AAT GCT GAT ACT GCT CCA ACA TCT CCT TGT CCT TCC ATA TCT TCC CAG AAC
ser thr met asn ala asp thr ala pro thr ser pro cys pro ser ile ser ser gln asn
61
91
TCA AGC TCC TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC AGC ATG TTC GAT CGG ACT TCC
ser ser ser cys ser ser phe gln asp gln lys ile ala ser met phe asp arg thr ser
121
151
AGA GTA CCC GCC AGC AGC ACT TCC TCA CCG GGG CTC CTC TTC ACA GAA CTG GCT GCT GCC
arg val pro ala ser ser thr ser ser pro gly leu leu phe thr glu leu ala ala ala
181
211
CTG GAT GCC GAA GGG GAA GGA ATC AGC GAA GTA CAA AGG AAA GCT GTC AGT GCA ATT CAC
leu asp ala glu gly glu gly ile ser glu val gln arg lys ala val ser ala ile his
241
271
AGC CTG CTA AGT TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA CCA GAG GTG AAG GTC AAA
ser leu leu ser ser his asp leu asp pro arg cys val lys pro glu val lys val lys
301
331
ATC GCC GCC CTT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT GCT TTG CCA CAG CTC TGT
ile ala ala leu tyr leu pro leu val gly ile ile leu asp ala leu pro gln leu cys
361
391
GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC TCG GAT GAA GAA CAA GAA
asp phe thr val ala asp thr arg arg tyr arg thr ser gly ser asp glu glu gln glu
421
451
GGA GCC GGT GCC ATT ACC CAG AAT GTG GCT CTG GCC ATA GCA GGG AAT AAT TTC AAT TTG
gly ala gly ala ile thr gln asn val ala leu ala ile ala gly asn asn phe asn leu
ref 2.1
481
511
AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG TAC AAC ATG CTG AAC GCG
lys thr ser gly ile val leu ser ser leu pro tyr lys gln tyr asn met leu asn ala
541
571
GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG AAA AAT GCT GAT CAG AGC
asp thr thr arg asn leu met ile cys phe leu trp ile met lys asn ala asp gln ser
601
631
CTC ATT AGG AAG TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC AAC AGG ATT TTA GAT CTA
leu ile arg lys trp ile ala asp leu pro ser thr gln leu asn arg ile leu asp leu
661
691
CTT TTC ATC TGT GTG TTA TGT TTT GAG TAT AAG GGA AAA CAG AGT TCT GAC AAA GTC AGT
leu phe ile cys val leu cys phe glu tyr lys gly lys gln ser ser asp lys val ser
721
751
ACC CAA GTC CTG CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG GAA GAG GCT TTG CTG CGT
thr gln val leu gln lys ser arg asp val lys ala arg leu glu glu ala leu leu arg
781
811
GGG GAA GGG GCC AGA GGG GAG ATG ATG CGC CGC CGG GCT CCA GGG AAC GAC CGA TTT CCA
gly glu gly ala arg gly glu met met arg arg arg ala pro gly asn asp arg phe pro

A

FIG. 4
1 of 7

841 871
GGC CTA AAT GAA AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT TGG CGG CAA GCT AAT GAG
gly leu asn glu asn leu arg trp lys lys glu gln thr his trp arg gln ala asn glu

901 931
AAG CTA GAT AAA ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG ATC AGT GGC AAT CTG GCT
lys leu asp lys thr lys ala glu leu asp gln glu ala leu ile ser gly asn leu ala

961 991
ACA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT ATC CAG GCG AGC TCG GCT
thr glu ala his leu ile ile leu asp met gln glu asn ile ile gln ala ser ser ala

1021 1051
CTG GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG CTG GTG AAT TCT CTG AAC
leu asp cys lys asp ser leu leu gly gly val leu arg val leu val asn ser leu asn

ref 3.1

1081 1111
TGT GAT CAG AGT ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA CTC CGT GCT CTC ATC GCC
cys asp gln ser thr thr tyr leu thr his cys phe ala thr leu arg ala leu ile ala

1141 1171
AAG TTT GGA GAC TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT TTC GAC CTA TGT CAC CAA
lys phe gly asp leu leu phe glu glu glu val glu gln cys phe asp leu cys his gln

1201 1231
GTC CTG CAC CAC TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC CAA GCC TGT GCC ACC CTT
val leu his his cys ser ser ser met asp val thr arg ser gln ala cys ala thr leu

1261 1291
TAC CTC CTC ATG AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT GCA AGA GTA AAG ATG CAA
tyr leu leu met arg phe ser phe gly ala thr ser asn phe ala arg val lys met gln

1321 1351
GTA ACC ATG TCC CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC TTT AAT GAA GAG CAC CTG
val thr met ser leu ala ser leu val gly arg ala pro asp phe asn glu glu his leu

1381 1411
AGA AGA TCC TTG AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC ACA GCC ATG CAG ATG ACT
arg arg ser leu arg thr ile leu ala tyr ser glu glu asp thr ala met gln met thr

1441 1471
CCT TTT CCC ACC CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT AGC ATC TTA TAT GAC ACA
pro phe pro thr gln val glu glu leu leu cys asn leu asn ser ile leu tyr asp thr

1501 1531
GTG AAA ATG AGG GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG GAT CTC ATG TAC AGA ATT
val lys met arg glu phe gln glu asp pro glu met leu met asp leu met tyr arg ile

1561 1591
GCC AAG AGT TAC CAG GCA TCT CCT GAT CTG CGG CTG ACC TGG CTC CAG AAC ATG GCA GAG
ala lys ser tyr gln ala ser pro asp leu arg leu thr trp leu gln asn met ala glu

1621 1651
AAA CAC ACC AAG AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC CTG GTG CAC GCC GCT GCG
lys his thr lys lys lys cys tyr thr glu ala ala met cys leu val his ala ala ala

A

FIG. 4
2 of 7

1681 1711
TTA GTG GCT GAG TAT CTG AGC ATG CTG GAG GAC CAC AGC TAC CTG CCC GTG GGC AGT GTC
leu val ala glu tyr leu ser met leu glu asp his ser tyr leu pro val gly ser val

1741 1771
AGC TTC CAG AAT ATT TCT TCC AAT GTG CTG GAG GAG TCT GTG GTC TCT GAG GAC ACC CTG
ser phe gln asn ile ser ser asn val leu glu glu ser val val ser glu asp thr leu

1801 1831
TCA CCT GAC GAG GAT GGG GTG TGC GCA GGC CAG TAC TTC ACC GAG AGT GGC CTG GTA GGC
ser pro asp glu asp gly val cys ala gly gln tyr phe thr glu ser gly leu val gly

1861 1891
CTC CTG GAG CAG GCC GCG GAG CTC TTC AGC ACG GGA GGC TTA TAT GAG ACA GTT AAT GAG
leu leu glu gln ala ala glu leu phe ser thr gly gly leu tyr glu thr val asn glu

1921 1951
GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA TTC CGG AAG CTG ACA CTC
val tyr lys leu val ile pro ile leu glu ala his arg glu phe arg lys leu thr leu

1981 2011
ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC AAG GAT CAT AAG AGA ATG
thr his ser lys leu gln arg ala phe asp ser ile val asn lys asp his lys arg met

2041 2071
TTT GGA ACC TAC TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT GGG GAT TTG GAT GAA CAG
phe gly thr tyr phe arg val gly phe phe gly ser lys phe gly asp leu asp glu gln

2101 2131
GAG TTT GTC TAC AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG ATC TCA CAT AGA CTA GAG
glu phe val tyr lys glu pro ala ile thr lys leu pro glu ile ser his arg leu glu

2161 2191
GCA TTT TAT GGT CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG ATT AAA GAC TCC ACT CCT
ala phe tyr gly gln cys phe gly ala glu phe val glu val ile lys asp ser thr pro

ref 4.1

2221 2251
GTG GAC AAA ACC AAG TTG GAT CCT AAC AAG GCC TAC ATA CAG ATC ACT TTT GTG GAG CCC
val asp lys thr lys leu asp pro asn lys ala tyr ile gln ile thr phe val glu pro

2281 2311
TAC TTT GAT GAG TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT GAG AAG AAT TTC AAC CTC
tyr phe asp glu tyr glu met lys asp arg val thr tyr phe glu lys asn phe asn leu

2341 2371
CGG AGG TTC ATG TAC ACC ACC CCG TTC ACC CTG GAG GGG CGG CCT CGG GGA GAG CTG CAT
arg arg phe met tyr thr thr pro phe thr leu glu gly arg pro arg gly glu leu his

2401 2431
GAG CAG TAC AGA AGG AAC ACA GTC CTG ACC ACT ATG CAC GCC TTC CCC TAC ATC AAG ACC
glu gln tyr arg arg asn thr val leu thr thr met his ala phe pro tyr ile lys thr

2461 2491
AGG ATC AGC GTC ATC CAG AAG GAG GAG TTT GTT TTG ACA CCG ATT GAA GTT GCC ATT GAA
arg ile ser val ile gln lys glu glu phe val leu thr pro ile glu val ala ile glu

A

FIG. 4
3 of 7

2521 2551
GAC ATG AAG AAG AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC CAG GAG CCG CCT GAT GCA
asp met lys lys lys thr leu gln leu ala val ala ile asn gln glu pro pro asp ala

2581 2611
AAG ATG CTT CAG ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT GTA AAT CAG GGA CCA CTG
lys met leu gln met val leu gln gly ser val gly ala thr val asn gln gly pro leu

2641 2671
GAA GTA GCC CAA GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA AAA CTC TAT CGA CAT CAC
glu val ala gln val phe leu ala glu ile pro ala asp pro lys leu tyr arg his his

2701 2731
AAC AAG TTG AGG TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT GGT GAA GCT GTA GAG AAA
asn lys leu arg leu cys phe lys glu phe ile met arg cys gly glu ala val glu lys

2761 2791
AAC AAG CGT CTC ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG GAA CTC AAA AAG AAC TAT
asn lys arg leu ile thr ala asp gln arg glu tyr gln gln glu leu lys lys asn tyr

2821 2851
AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA ATT CCA GAA CTG TAC AAG
asn lys leu lys glu asn leu arg pro met ile glu arg lys ile pro glu leu tyr lys

2881 2911
CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC AGA TCT AGT TTC AGG AAA
pro ile phe arg val glu ser gln lys arg asp ser phe his arg ser ser phe arg lys

2941 2971
TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA GAA AAG CCA TCT TCA TTC GTG GAG ACT GTG
cys glu thr gln leu ser gln gly ser OCH

ref 5.1

3001 3031
GCC CTG CAA CCC TGG AGA AGG ACT TGC TGG TAC TTA AAA AAT GGG ACA TTT GCC ACC CAG

3061 3091
GAC TGA CTG TAC ACT CCC TGA TCA GCC AGC ACT CTG GAA GCT TTG GGA TCC CAG GAA CCA

3121 3151
TGG AAT TAT TCC CAA ATG GAC TCT GAC CAG ATT TTT GCC ATA CTG GGG GGT GGC GGG ATG

3181 3211
GAG GAT GGG TAC TCA GGC ATG ACT GCG TAT TTA TTA AAG TGT GTT TTT CCA CAA TGT ACC

3241 3271
AAA CAA GGC ATA AGC AGC TTC TCC TGC TGA CTG GCC AAT CAC TGC CCA TCT GAG AGA TGA

3301 3331
TTT CCT CTG GCC CAT ATT TGA ATT TAT TGG AGT AAC TCA AAT TGC CTG AGG AAA AAT GGA

3361 3391
AAA ATT ATC CAC CAG TCG ATT CAA ACT GAA TTT CAC TCT TTA TAG GAA GGC AGG GCA AAC

3421 3451
TTG TAG GAG TAC GAA ACA TTT TCA ATA AAT CTA CAA AGG GAA GCC TTA CTA CAA TTC CAA

3481 3511

A

FIG. 4
4 of 7

AAA TCA TCA TGG TTG GAA ATT TGG GAG GAG ATT ATT TGT GAA CTT GTT ACC CTT TTG GTA

3541 3571
ATG GTG GAC TAA TTG CTG TAT AGT TAT TTT TGT TTT ATT ATT ACT GTT ACA TTA ATT TAA

3601 3631
CAT GCA TTT ATA GAA GAA TAC ATT CAA AGC ACT GAT GTA GGA GAT ACA CGG TAC TTG GAG

3661 3691
CAG TCA GCC AAA AAT CAC AGA TAC TGC TTT CAC TTA AAT GGA AAC AAT TCT CCG ATA ATG

3721 3751
CTT TGC TTT TTT TCT TAT GTC ACT CTT GTG TAC TAT CTA TTT TTC TCC TCT CTG GGA CCA

3781 3811
AGT TTC TTT TTA TAA AGC AAT AAT ATC TCT GTT TTC ATT TCA GAA CAT TGT GCT GTC TGT

3841 3871
CAG CAT ATG TAT ATC AGC TAC AAA ATA TAT TCA ACT TTG ACT TCT TTT GAC AAA GGA CTT

3901 3931
TAG GAA AAG GAG GAA CAA AGA CAT TAT TTG AGA ATT AAA TTA TAT ATT TTT AAT ATG ACT

3961 3991
GTG ACC TTG ACT GAT AAT AAA GAT GTA ATA AGA ATT GCA AGC TAA AAA AAA AAA AAA AAA

4021
AAC TCG

References

BAC sequences of Human CLASP 5

Ref 1.1

Sequence of BAC19 using primer HC5S11, which spans nucleotides 3-22 of the cDNA. Exon sequence is underlined and represents nucleotides 32-57.

CTCTCTGTCTTCATATCTTCCAGGTTATAAAGNATTATTTACTAAAAGAANATTCANGC
TATTTCATTTAACTAGCTCAGTTTAATCATGTATTTCCTATAAAGGTTAGTCTTATTAAT
TTGACAAAACAATCAAACAATTCAAACCAGATCAAGTATGCTACCCTGAAGTTACACC
ACTAGCTAAGAATTAACAATCTAAGTAATTGGTTTCTCCCCAGGCTCAAGGCTCCCTGA
TCAGGTTAAGTAAAGCCAAGAATCCAATAAGCCCTATGAAATTTAGAAACTCATAGAA
AAGTCTCAAATCTTCTTGTCTGACATTAGCCAATTGTTATATTATGCAAATAGAGGATT
NCAAGTAAATAAGTTTGGAACCTGTTTACCAGGTTTTTGCAGCAGNCCTCTAAGAGCTT
AACTGGTCATGCATTGAATGCCGAGAGCAAAGAGGAATGGAGAGGGGNTGTAAGNGG
TTCCAATNTTACTGGAACCCACCACTATCTTTNGAAGTCTTGATACTTAACTGNGTGTA
GNCTCTTTAGGCCTNTANTAANTAGAATCTATATGGATTCGTGTTCTGTCNGCAAGNAG
TGCCTATGAAA

A

FIG. 4
5 of 7

Ref 2.1

Sequence of BAC19 using primer HC5AS10b, which spans nucleotides 560-580 of the cDNA. Exon sequence is underlined and represents nucleotides 510-553.

TGCGAGTAGTGTCCGCGTTCAGCATGTTGTACTGCTTATAGGGCTGAAGGGAGGCACG
ATTGGGGGATGGAGGCCAGGGAAGAAGTCAAGCAACAGAAAAATTTGAGGCTTAACA
GTCAAGCAACAGAAAAATTCAAAGTGTTCTCTTAAAATACCATGACTGTACATCACTG
CTAGGCTGGAGATCTATTGCCAGTAGCCCTGCCTTCCCTAGGCAGGGGAAGCTGTGTT
CTTTGAGTAGCGCTACTCAGCAAAGAGGCTCACCTGGGGCAGTATTTGAGCTAGGCTT
TCAGCCACCGTATCTGAGTACCTCTGTCTTANGAGCAGTGTGGCCTGGTGATCACCCCT
GGGCCTTGATCATGCGTGCTGCAATCCCAGTGATACAAAGAGGCTTTCATGCTGCTAA
GATCTCCAAGTATTTCTCCTTCGTGCTGGGCAGCAGAGGGTTAGACTTNCAGGGGAGA
AGGAAACTGGCTGGGTGCCATGAATAANCTTGCTGTTCAAGANTTAACTTCTTTGTTAC
ATAAGNGCAAAGGTATAACATAAAGGGNCATGAACTGCTCAACNAAATTNATCAAAT
CCATGTTTGTGGGAGTTCTTTTGTNATNGGAAGTTTAACCCCTAA

Ref 3.1

Sequence of BAC13 using primer C5S3, which spans nucleotides 1086-1105 of the cDNA. Exon sequence is underlined and represents nucleotides 1110-1120.

CCCNGCTCTTTTTGGCAANGTAANCTTGGGATGCTTGTTTTCTTCCTCTTAATTAAGAG
NAAGANTTTTTTTAGCTTCATACTTCTCTCTTCAGGGGGACCAAAAGTCACAGAGCATA
TTAAGTGGCANAACCCCNAAGGTCTTAAGTCTTCCTAGGAAGAAAGCAGATGCCCTGA
TTCTGTGGGAAGCCACCATGGAGAGGAAAAGCAGTGGCTCCCATATTTGAAGTGNGGA
CCTAACTCTAGAAAGTTTAAAANGGCCATTTGCTGAAGGGCTATGACATGAGAACAGA
GATCAACTGAGTGACTTAGCAANTTCACTCTTTCTCTGTAANACCTCTGGTGAGTGAGA
NTAAATCCTNTATGTGACGCCCATTAGTCTTACAAAANGTCATGCCNTAAAATGCCAN
GAAGGNCAGAAATGAATTTCTCACCGCCNGAGGAATGAGGATTATNCTGGGGGGACA
TGCANAAATATTNNNCCCCCNATTTATTNATTTATTTATTTTTGAGACNGAGTNTCGNT
CTAATCGCCCCCAGGCTGGNAGGTGGNAGGTGGTTCCCATCTTNAANCTTANNTNGGA
AGGNCCTCTTTGNGCCCCNGGGGGGNGNAAAGNGAATTCCCTAAATGCCTNCANNCCC
CTCCCTGGANGTTATTTGGGGGNNTTNTAAAGGGCNGTGGCNG

Ref 4.1

Sequence of BAC13 using primer C5S7, which spans nucleotides 2196-2205 of the cDNA. . Exon sequence is underlined and represents nucleotides 2225-2231.

ACAAAAACTAACCATCANTCTCTAAATCCCAACAANCTTTTTTTAAGAATACCTAANG
AGCTCAACNAGGGGGACTNTCCAANGCACTTAAATGCAGNCAAACNACNCCNNCAAG
AGNGGCAACTACTAATGGGGCANATCTNAAAGAAAATATAGNCAAAGGNNGGAATCA
TAATAGGAGCNACCACTTANGAAGCACCAACTGGGGACCTGGAACTGNATNAGGNCC
TCTACATACATCATNNNATANCATCCTGCAACGACCCCTGGAAGGAGANAGANGGNA

A

TTCCTANNNTAGAGANGAGANAACTGGGGACATGGGAAGAGGNAAGCGAAGGGTTCA
AGGGGANGNAAGCGAGCAGANNCCAGGGNCTCANACTNGNGGGGNNTGGGGGGNTN
CTGNNNCCCTACNCTTNGNANGAACAGNGNNGTTGANNTGGCTTTNGANTA

Ref 5.1

Sequence of BAC13 using primer 122047F1, which spans nucleotides 3537-3556 of the cDNA. Exon sequence is underlined and represents nucleotides 3000-3492. This region does not contain a intron in this region

CCANNAGATTNTTGNAACGNNGGTAGGCTTCCTTTGTAGATTTATTGAAAATGTTTCGT
ACTTCTACAAGTTTGCCCTGCCTTCCTATAAAGAGTGAAANTCANTTTGAATCGACTGG
TGGATAATTNTTCCATTTTTCCTCAGGCAATTTNGAGTTACTCCAATAAATTCAAATAT
GGGCCAGAGGAAATCATCTTTCAGATGGGCAGTGATTGGCCAGTCAGCAGGAGAAGC
TGCTTATGCCTTGTTTGGTACATTGTGGAAAAACACACTTTAATAAATACGCANTCATG
CCTGAGTACCCATCCTCCATCCCGCCACCCCCCAGTATGGCAAAAATCTGGTCAGAGT
CCATTTGGGAATAATTCCATGGTTCCTGGGATCCCAAAGCTTCCAGAAGTGCTGGCTG
ATCAANGGAGTGTACAGTCAGTCCTGGGTGGCAAAAATGTCCCATTTTTTAAGTACCA
AGCAAAGGTTCCTTCTTNCAAGGGTTNCTAGGGCC

A

Figure
Multiple sequence alignment of Human CLASP proteins with intron/exon borders indicated by a vertical line. Numbers in right margin correspond to References

```
HC2A    ------------------------------------------------------------
KIAA    ASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat     ------------------------------------------------------------
HC4     ------------------------------------------------------------
HC1     ------------------------------------------------------------
HC3     ------------------------------------------------------------
HC5     ------------------------------------------------------------

HC2A    ------------------------------------------------------------
KIAA    FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
rat     ------------------------------------------------------------
HC4     ------------------------------------------------------------
HC1     ------------------------------------------------------------
HC3     ------------------------------------------------------------
HC5     ------------------------------------------------------------

HC2A    ------------------------------------------------VLHHHQNPEFYDEIK
KIAA    KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPEFYDEIK
rat     ------------------------------------------------------------
HC4     ------------------------------------------------------------
HC1     ------------------------------------------------------------
HC3     ------------------------------------------------------------
HC5     ------------------------------------------------------------

HC2A    IELPTQLHEKHHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA    IELPTQLHEKHHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat     ------------------------------------------------------------
HC4     ------------------------------------------------------------
HC1     ------------------------------------------------------------
HC3     ------------------------------------------------------------
HC5     ------------------------------------------------------------

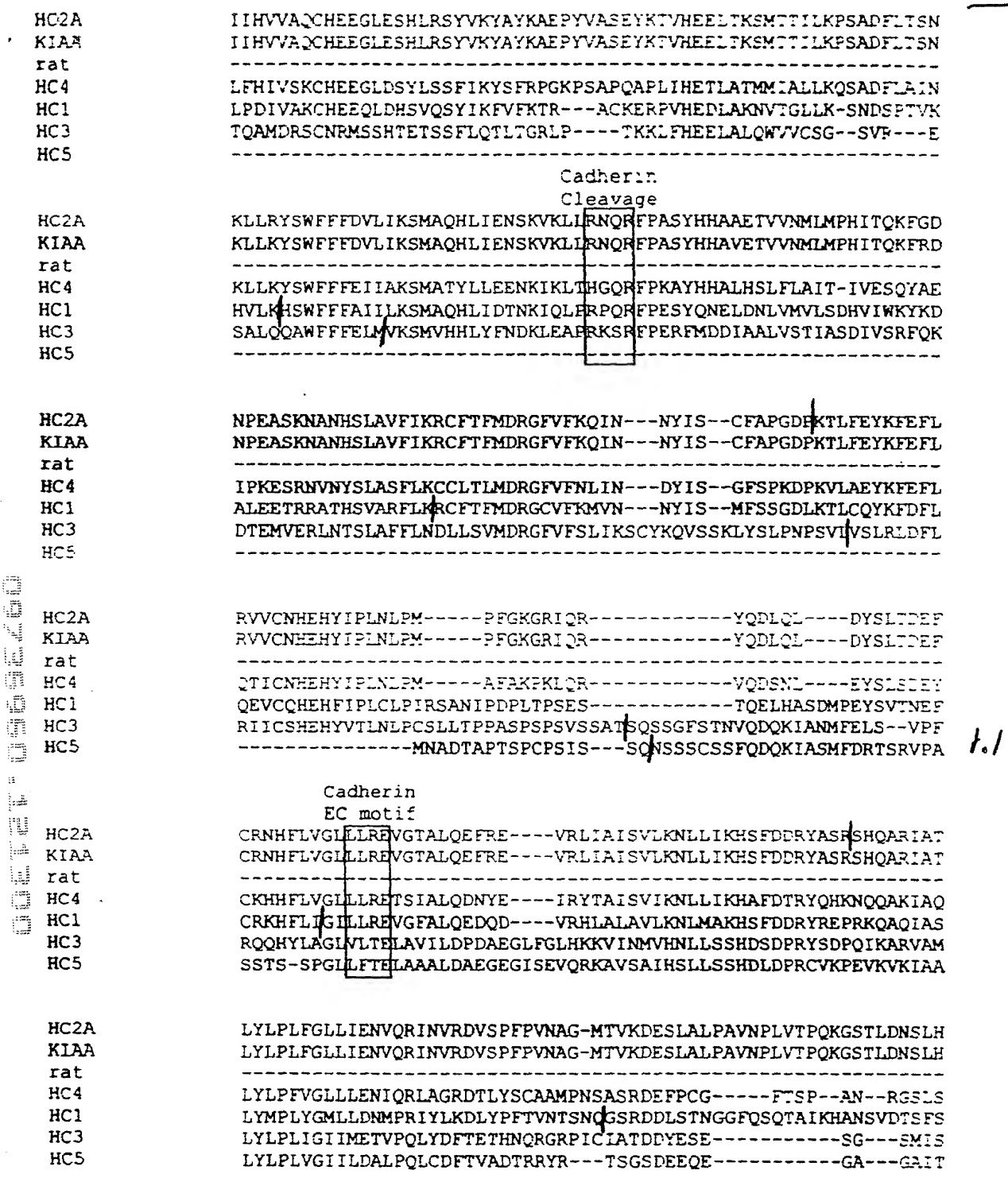
HC2A    PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
KIAA    PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
rat     ------------------------------------------------------------
HC4     ------------------------------------------------------------
HC1     ------------------------------------------------------------
HC3     ----------------------------------------GPGPARSTVSISLISNSARV
HC5     ------------------------------------------------------------

HC2A    QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA    QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat     ------------------------------------------------------------
HC4     ----------------------MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1     ---------------------------MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3     NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5     ------------------------------------------------------------
```

B

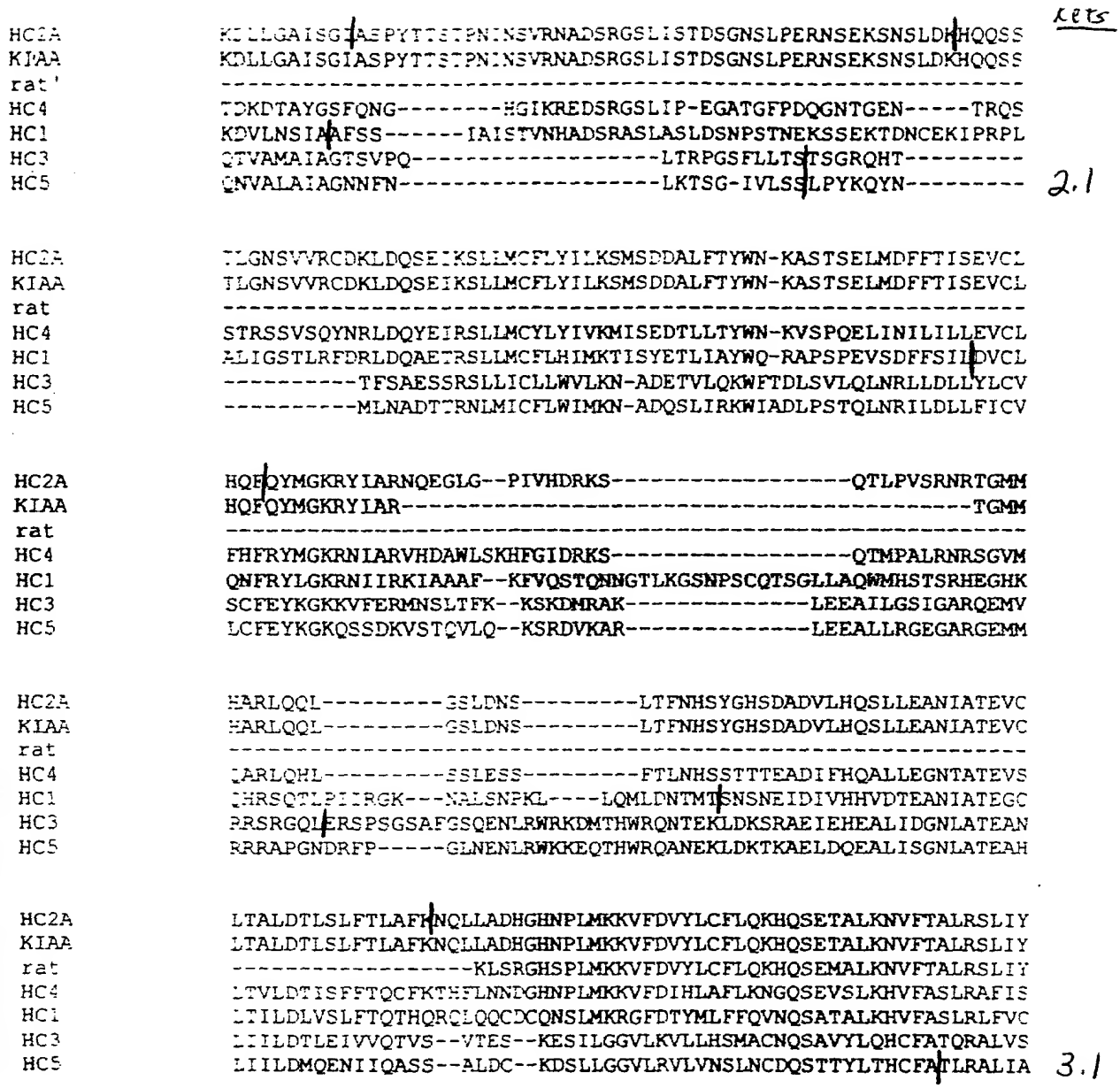
FIG. 4
1 of 4

Refs



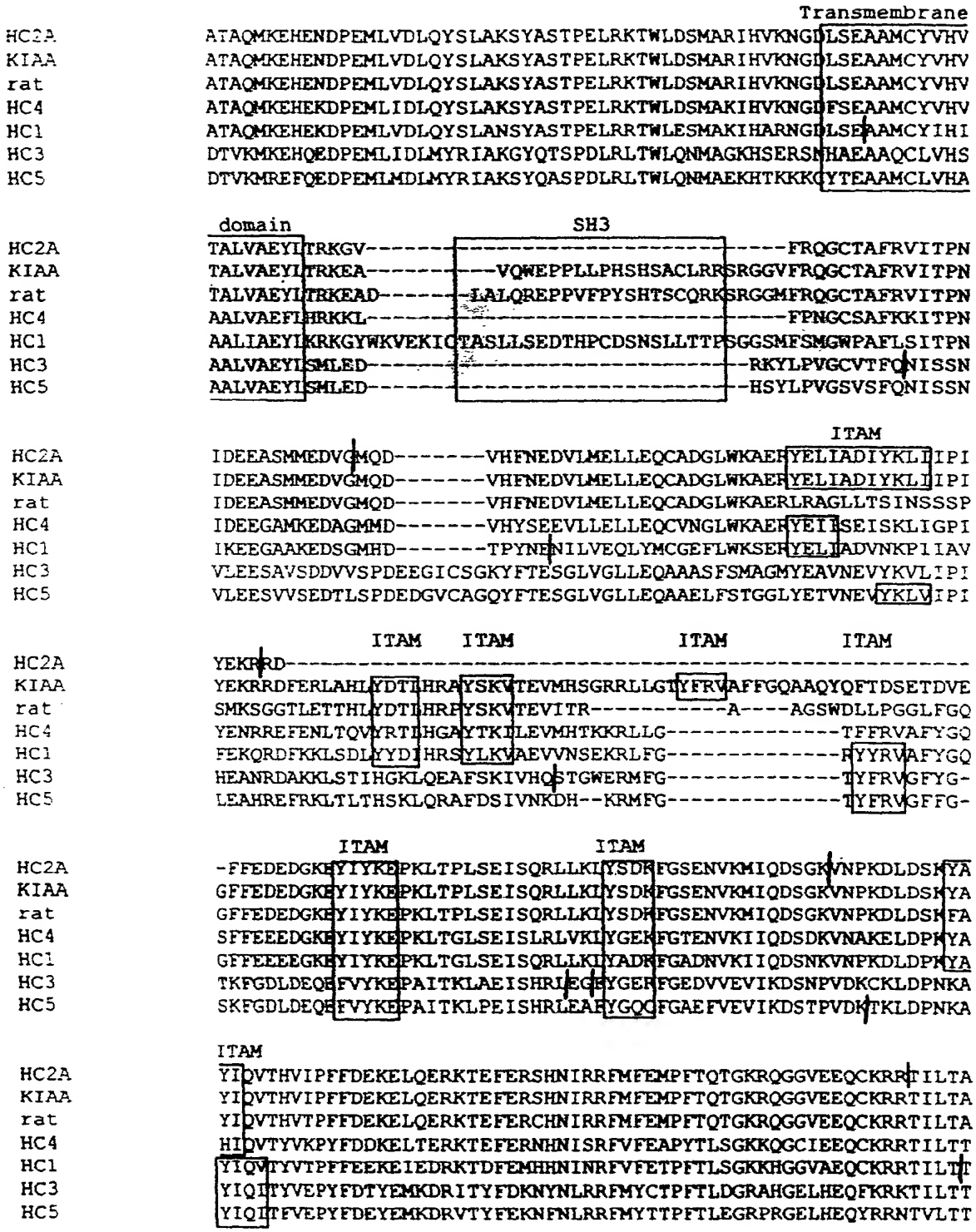
B

FIG. 4
2 of 4


HC2A
KIAA
rat'
HC4
HC1
HC3
HC5
HC2A
KIAA
rat
HC4
HC1
HC3
HC5
HC2A
KIAA
rat
HC4
HC1
HC3
HC5
HC2A
KIAA
rat
HC4
HC1
HC3
HC5
HC2A
KIAA
rat
HC4
HC1
HC3
HC5
2.1
3.1

B

FIG. 4
3 of 4


Transmembrane
HC2A ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHV
KIAA ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHV
rat ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHV
HC4 ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLDSMAKIHVKNGDFSEAAMCYVHV
HC1 ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLESMAKIHARNGDLSEAAMCYIHI
HC3 DTVKMKEHQEDPEMLIDLMYRIAKGYQTSPDLRLTWLQNMAGKHSERSNHAEAAQCLVHS
HC5 DTVKMREFQEDPEMLMDLMYRIAKSYQASPDLRLTWLQNMAEKHTKKKQYTEAAMCLVHA
domain
SH3
HC2A TALVAEYLTRKGV----------FRQGCTAFRVITPN
KIAA TALVAEYLTRKEA----------VQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRVITPN
rat TALVAEYLTRKEAD----------LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4 AALVAEFLHRKKL----------FPNGCSAFKKITPN
HC1 AALIAEYIKRKGYWKVEKICTASLLSEDTHPCDSNSLLTTPSGGSMFSMGWPAFLSITPN
HC3 AALVAEYLSMLED----------RKYLPVGCVTFQNISSN
HC5 AALVAEYLSMLED----------HSYLPVGSVSFQNISSN
ITAM
HC2A IDEEASMMEDVGMQD--------VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIIPI
KIAA IDEEASMMEDVGMQD--------VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIIPI
rat IDEEASMMEDVGMQD--------VHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSSP
HC4 IDEEGAMKEDAGMMD--------VHYSEEVLLELLEQCVNGLWKAERYEISEISKLIGPI
HC1 IKEEGAAKEDSGMHD--------TPYNENILVEQLYMCGEFLWKSERYELIADVNKPIIAV
HC3 VLEESAVSDDVVSPDEEGICSGKYFTESGLVGLLEQAAASFSMAGMYEAVNEVYKVLIPI
HC5 VLEESVVSEDTLSPDEDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKLVIPI
ITAM ITAM ITAM ITAM
HC2A YEKRRD----------
KIAA YEKRRDFERLAHLYDTLHRAYSKVTEVMHSGRRLLGLYFRVAFFGQAAQYQFTDSETDVE
rat SMKSGGTLETTHLYDTLHRFYSKVTEVITR----------A----AGSWDLLPGGLFGQ
HC4 YENRREFENLTQVYRTLHGAYTKILEVMHTKKRLLG----------TFFRVAFYGQ
HC1 FEKQRDFKKLSDLYYDIHRSYLKVAEVVNSEKRLFG----------HYYRVAFYGQ
HC3 HEANRDAKKLSTIHGKLQEAFSKIVHQSTGWERMFG----------TYFRVGFYG-
HC5 LEAHREFRKLTLTHSKLQRAFDSIVNKDH--KRMFG----------TYFRVGFFG-
ITAM ITAM
HC2A -FFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA
KIAA GFFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA
rat GFFEDEDGKEYIYKEPKLTPLSEISQRLLKLYSDKFGSENVKMIQDSGKVNPKDLDSKFA
HC4 SFFEEEDGKEYIYKEPKLTGLSEISLRLVKLYGEKFGTENVKIIQDSDKVNAKELDPKYA
HC1 GFFEEEEGKEYIYKEPKLTGLSEISQRLLKLYADKFGADNVKIIQDSNKVNPKDLDPKYA
HC3 TKFGDLDEQEFVYKEPAITKLAEISHRLEGEYGEKFGEDVVEVIKDSNPVDKCKLDPNKA
HC5 SKFGDLDEQEFVYKEPAITKLPEISHRLEAEYGQQFGAEFVEVIKDSTPVDKTKLDPNKA
ITAM
HC2A YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
KIAA YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
rat YIQVTHVTPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
HC4 HIQVTYVKPYFDDKELTERKTEFERNHNISRFVFEAPYTLSGKKQGCIEEQCKRRTILTT
HC1 YIQVTYVTPFFEEKEIEDRKTDFEMHHNINRFVFETPFTLSGKKHGGVAEQCKRRTILTT
HC3 YIQITYVEPYFDTYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAHGELHEQFKRKTILTT
HC5 YIQITFVEPYFDEYEMKDRVTYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLTT
4.1

B

FIG. 4
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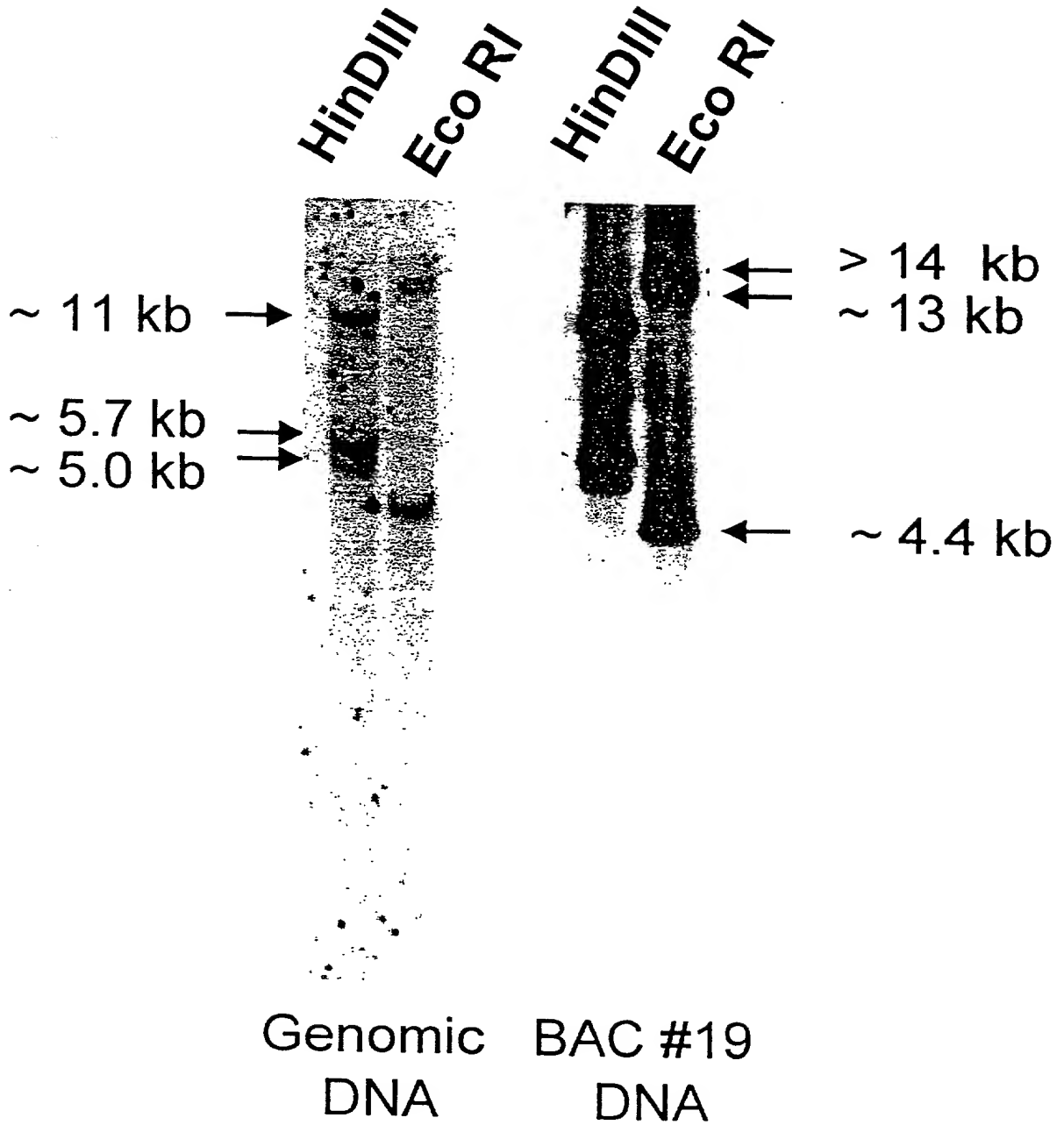
HinDIII
Eco RI
HinDIII
Eco RI
~ 11 kb
~ 5.7 kb
~ 5.0 kb
> 14 kb
~ 13 kb
~ 4.4 kb
Genomic DNA
BAC #19 DNA

FIG. 5

-111
CGGTAACCGCCATTTTGTCTCCTGTAACAATTTACGCGCCGTGTAACTGTGAATCTTTCAAAGCCTCAGTTTTATGACC
CTGTGGAGCCAGTGGACTTTGAAGGACTTCTG -1

1/1 31/11
ATG ACA CAC CTG AAC AGC CTG GAT GTG CAG CTT GCC CAG GAG CTC GGG GAC TTC ACT GAT
Met thr his leu asn ser leu asp val gln leu ala gln glu leu gly asp phe thr asp
61/21 91/31
GAC GAC TTG GAC GTG GTG TTC ACG CCA AAG GAA TGT AGG ACT TTG CAG CCC TCT TTG CCG
asp asp leu asp val val phe thr pro lys glu cys arg thr leu gln pro ser leu pro
121/41 151/51
GAG GAA GGG GTT GAA CTG GAC CCT CAT GTC AGG GAC TGT GTT CAG ACC TAC ATC CGT GAG
glu glu gly val glu leu asp pro his val arg asp cys val gln thr tyr ile arg glu
181/61 211/71
TGG CTA ATC GTG AAC CGG AAA AAC CAA GGA AGT CCA GAA ATC TGT GGC TTT AAA AAG ACT
trp leu ile val asn arg lys asn gln gly ser pro glu ile cys gly phe lys lys thr
241/81 271/91
GGA TCT CGA AAA GAT TTT CAC AAG ACG CTT CCG AAA CAG ACG TTT GAG TCG GAA ACC TTG
gly ser arg lys asp phe his lys thr leu pro lys gln thr phe glu ser glu thr leu
301/101 331/111
GAG TGC AGT GAA CCC GCT GCT CAG GCA GGC CCC CGC CAC TTA AAC GTG CTG TGC GAC GTG
glu cys ser glu pro ala ala gln ala gly pro arg his leu asn val leu cys asp val
361/121 391/131
TCT GGG AAA GGC CCC GTC ACT GCC TGT GAC TTT GAC CTC CGC AGC CTG CAG CCT GAC AAG
ser gly lys gly pro val thr ala cys asp phe asp leu arg ser leu gln pro asp lys
421/141 451/151
CGG CTA GAA AAC CTC CTG CAG CAA GTG AGT GCC GAG GAC TTT GAG AAG CAG AAC GAG GAG
arg leu glu asn leu leu gln gln val ser ala glu asp phe glu lys gln asn glu glu
481/161 511/171
GCC CGG AGG ACC AAC AGG CAG GCC GAG CTC TTT GCC CTT TAC CCA TCA GTG GAC GAG GAG
ala arg arg thr asn arg gln ala glu leu phe ala leu tyr pro ser val asp glu glu
541/181 571/191
GAT GCT GTG GAA ATA CGT CCA GTA CCA GAA TGT CCC AAG GAA CAC CTG GGC AAC AGA ATA
asp ala val glu ile arg pro val pro glu cys pro lys glu his leu gly asn arg ile
601/201 631/211
TTG GTC AAG TTG CTG ACC TTG AAG TTC GAG ATT GAA ATT GAG CCC CTG TTT GCC AGC ATT
leu val lys leu leu thr leu lys phe glu ile glu ile glu pro leu phe ala ser ile
661/221 691/231
GCC CTC TAC GAT GTT AAA GAA AGG AAA AAG ATC TCA GAA AAT TTT CAC TGT GAC CTG AAC
ala leu tyr asp val lys glu arg lys lys ile ser glu asn phe his cys asp leu asn
721/241 751/251
TCT GAC CAG TTC AAA GGA TTT CTG CGA GCT CAC ACG CCT TCA GTG GCC GCA TCA AGT CAG
ser asp gln phe lys gly phe leu arg ala his thr pro ser val ala ala ser ser gln
781/261 811/271
GCG AGA TCT GCA GTC TTC TCA GTC ACC TAC CCG TCC TCA GAC ATC TAC CTG GTA GTC AAG
ala arg ser ala val phe ser val thr tyr pro ser ser asp ile tyr leu val val lys
841/281 871/291
ATT GAA AAA GTC CTG CAG CAG GGA GAT ATT GGA GAC TGT GCA GAG CCC TAC ACG GTT ATC
ile glu lys val leu gln gln gly asp ile gly asp cys ala glu pro tyr thr val ile
901/301 931/311
AAA GAA AGT GAT GGT GGA AAG AGT AAA GAA AAG ATT GAA AAA CTA AAA CTC CAA GCT GAA
lys glu ser asp gly gly lys ser lys glu lys ile glu lys leu lys leu gln ala glu
961/321 991/331
TCC TTC TGC CAG CGT TTG GGG AAA TAC CGG ATG CCC TTT GCC TGG GCA CCC ATA AGC TTA
ser phe cys gln arg leu gly lys tyr arg met pro phe ala trp ala pro ile ser leu

A

FIG. 6

1021/341 1051/351
TCA AGC TTC TTC AAT GTC TCC ACC CTT GAG AGG GAG GTA ACT GAT GTG GAC TCT GTG GTT
ser ser phe phe asn val ser thr leu glu arg glu val thr asp val asp ser val val
1081/361 1111/371
GGG AGA AGC CCA GTG GGT GAA CGG AGG ACA TTG GCC CAA TCT AGA AGG CTT TCT GAA AGA
gly arg ser pro val gly glu arg arg thr leu ala gln ser arg arg leu ser glu arg
1141/381 1171/391
GCC CTC TCC TTG GAG GAA AAT GGG GTT GGA TCC AAC TTC AAA ACC TCC ACT CTG AGC GTT
ala leu ser leu glu glu asn gly val gly ser asn phe lys thr ser thr leu ser val
1201/401 1231/411
AGC AGC TTT TTC AAG CAG GAA GGA GAT CGC CTT AGC GAT GAA GAC TTA TTC AAG TTT TTA
ser ser phe phe lys gln glu gly asp arg leu ser asp glu asp leu phe lys phe leu
1261/421 1291/431
GCT GAC TAC AAA AGA TCA TCA TCC TTA CAG AGA CGA GTC AAG TCA ATT CCA GGC TTG CTA
ala asp tyr lys arg ser ser ser leu gln arg arg val lys ser ile pro gly leu leu
1321/441 1351/451
AGA CTG GAG ATT TCT ACA GCT CCA GAG ATC ATC AAT TGC TGT CTG ACT CCT GAA ATG CTG
arg leu glu ile ser thr ala pro glu ile ile asn cys cys leu thr pro glu met leu
1381/461 1411/471
CCC GTG AAA CCC TTT CCT GAA AAC CGG ACA CGC CCG CAC AAA GAG ATT TTG GAA TTT CCA
pro val lys pro phe pro glu asn arg thr arg pro his lys glu ile leu glu phe pro
1441/481 1471/491
ACA CGA GAA GTA TAT GTC CCT CAC ACT GTG TAC AGA AAC CTT CTC TAT GTC TAC CCA CAG
thr arg glu val tyr val pro his thr val tyr arg asn leu leu tyr val tyr pro gln
1501/501 1531/511
AGG CTG AAC TTT GTA AAC AAA CTA GCA TCA GCC CGG AAC ATT ACA ATA AAG ATC CAG TTT
arg leu asn phe val asn lys leu ala ser ala arg asn ile thr ile lys ile gln phe
1561/521 1591/531
ATG TGT GGA GAA GAT GCT AGC AAT GCG ATG CCG GTC ATC TTT GGA AAA TCC AGC GGG CCT
met cys gly glu asp ala ser asn ala met pro val ile phe gly lys ser ser gly pro
1621/541 1651/551
GAA TTT CTG CAG GAA GTG TAC ACA GCT GTT ACA TAC CAT AAT AAG TCT CCT GAC TTT TAT
glu phe leu gln glu val tyr thr ala val thr tyr his asn lys ser pro asp phe tyr
1681/561 1711/571
GAA GAA GTG AAA ATT AAG CTC CCC GCT AAG CTC ACA GTA AAT CAC CAC CTC CTG TTC ACC
glu glu val lys ile lys leu pro ala lys leu thr val asn his his leu leu phe thr
1741/581 1771/591
TTC TAC CAT ATC AGC TGT CAG CAG AAG CAA GGA GCC TCC GTG GAA ACT CTC CTG GGA TAT
phe tyr his ile ser cys gln gln lys gln gly ala ser val glu thr leu leu gly tyr
1801/601 1831/611
TCA TGG CTG CCA ATT CTC TTA AAT GAA CGT CTT CAA ACT GGA TCC TAC TGT CTC CCA GTT
ser trp leu pro ile leu leu asn glu arg leu gln thr gly ser tyr cys leu pro val
1861/621 1891/631
GCC TTG GAA AAA TTG CCA CCC AAC TAC TCC ATG CAT TCT GCT GAG AAA GTC CCA TTA CAG
ala leu glu lys leu pro pro asn tyr ser met his ser ala glu lys val pro leu gln
1921/641 1951/651
AAT CCT CCC ATT AAG TGG GCT GAA GGA CAT AAG GGA GTA TTT AAT ATT GAA GTG CAA GCT
asn pro pro ile lys trp ala glu gly his lys gly val phe asn ile glu val gln ala
1981/661 2011/671
GTT TCT TCT GTA CAC ACC CAG GAC AAC CAC CTG GAG AAG TTC TTC ACC CTC TGC CAC TCC
val ser ser val his thr gln asp asn his leu glu lys phe phe thr leu cys his ser
2041/681 2071/691
CTG GAG AGC CAG GTG ACC TTC CCC ATC CGC GTG CTG GAT CAG AAA ATC AGC GAG ATG GCG
leu glu ser gln val thr phe pro ile arg val leu asp gln lys ile ser glu met ala
2101/701 2131/711
CTG GAG CAT GAG CTG AAG CTC AGC ATC ATC TGC CTG AAC TCC TCC CGC CTG GAG CCG CTC
leu glu his glu leu lys leu ser ile ile cys leu asn ser ser arg leu glu pro leu

A

FIG. 6
2 of 6

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2161/721                                    2191/731
GTG CTC TTC CTG CAC CTG GTG CTG GAC AAG CTC TTC CAG CTG TCC GTG CAG CCC ATG GTC
val leu phe leu his leu val leu asp lys leu phe gln leu ser val gln pro met val
2221/741                                    2251/751
ATC GCT GGC CAG ACA GCC AAC TTC TCC CAG TTT GCC TTC GAG TCC GTG GTG GCC ATC GCC
ile ala gly gln thr ala asn phe ser gln phe ala phe glu ser val val ala ile ala
2281/761                                    2311/771
AAC AGT CTG CAC AAC AGC AAG GAC CTG AGC AAG GAC CAG CAT GGG AGG AAC TGC CTG CTG
asn ser leu his asn ser lys asp leu ser lys asp gln his gly arg asn cys leu leu
2341/781                                    2371/791
GCT TCC TAC GTG CAC TAC GTC TTC CGC CTG CCA GAG GTG CAA AGG GAT GTG CCC AAG TCA
ala ser tyr val his tyr val phe arg leu pro glu val gln arg asp val pro lys ser
2401/801                                    2431/811
GGC GCT CCC ACT GCC CTC CTA GAC CCT CGG AGC TAC CAC ACG TAT GGC CGC ACA TCA GCT
gly ala pro thr ala leu leu asp pro arg ser tyr his thr tyr gly arg thr ser ala
2461/821                                    2491/831
GCT GCT GTG AGT TCA AAG CTG CTG CAG GCC CGG GTG ATG AGC AGC AGT AAC CCA GAC CTC
ala ala val ser ser lys leu leu gln ala arg val met ser ser ser asn pro asp leu
2521/841                                    2551/851
GCG GGG ACA CAC TCC GCA GCA GAC GAG GAA GTG AAG AAC ATC ATG TCT TCA AAG ATC GCC
ala gly thr his ser ala ala asp glu glu val lys asn ile met ser ser lys ile ala
2581/861                                    2611/871
GAT CGC AAC TGC AGC CGA ATG TCT TAC TAT TGC TCT GGC AGT AGT GAT GCT CCA AGT TCA
asp arg asn cys ser arg met ser tyr tyr cys ser gly ser ser asp ala pro ser ser
2641/881                                    2671/891
CCT GCA GCC CCA AGG CCA GCC AGC AAA AAG CAT TTC CAT GAG GAG CTT GCC CTT CAG ATG
pro ala ala pro arg pro ala ser lys lys his phe his glu glu leu ala leu gln met
2701/901                                    2731/911
GTG GTC AGC ACC GGA ATG GTG AAA AGC ATG GCC CAG CAC GTA CAT AAC ATG GAC AAA CGG
val val ser thr gly met val lys ser met ala gln his val his asn met asp lys arg
2761/921                                    2791/931
GAC AGT TTT CGG AGG ACT CGT TTT TCT GAC CGT TTC ATG GAT GAC ATA ACT ACT ATT GTT
asp ser phe arg arg thr arg phe ser asp arg phe met asp asp ile thr thr ile val
2821/941                                    2851/951
AAT GTG GTC ACC TCG GAA ATT GCA GCC CTT TTA GTA AAA CCA CAG AAG GAA AAT GAA CAG
asn val val thr ser glu ile ala ala leu leu val lys pro gln lys glu asn glu gln
2881/961                                    2911/971
GCG GAA AAG ATG AAC ATC AGC CTG GCT TTC TTC TTG TAT GAC CTT CTC TCC CTC ATG GAT
ala glu lys met asn ile ser leu ala phe phe leu tyr asp leu leu ser leu met asp
2941/981                                    2971/991
CGG GGC TTT GTG TTT AAC CTC ATC AGA CAT TAT TGC AGC CAG CTG TCA GCC AAG CTC AGT
arg gly phe val phe asn leu ile arg his tyr cys ser gln leu ser ala lys leu ser
3001/1001                                   3031/1011
AAC CTT CCA ACG CTC ATT TCC ATG AGG CTA GAG TTC CTG AGA ATC CTC TGT AGC CAT GAG
asn leu pro thr leu ile ser met arg leu glu phe leu arg ile leu cys ser his glu
3061/1021                                   3091/1031
CAT TAC CTC AAT CTG AAC CTT TTT TTT ATG AAT GCT GAT ACT GCT CCA ACA TCT CCT TGT
his tyr leu asn leu asn leu phe phe met asn ala asp thr ala pro thr ser pro cys
3121/1041                                   3151/1051
CCT TCC ATA TCT TCC CAG AAC TCA AGC TCC TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC
pro ser ile ser ser gln asn ser ser ser cys ser ser phe gln asp gln lys ile ala
3181/1061                                   3211/1071
AGC ATG TTC GAT CTG ACT TCC GAG TAC CGC CAG CAG CAC TTC CTC ACC GGG CTC CTC TTC
ser met phe asp leu thr ser glu tyr arg gln gln his phe leu thr gly leu leu phe
3241/1081                                   3271/1091
ACA GAA CTG GCT GCT GCC CTG GAT GCC GAA GGG GAA GGA ATC AGC AAA GTA CAA AGG AAA
thr glu leu ala ala ala leu asp ala glu gly glu gly ile ser lys val gln arg lys
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FIG. 6
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3301/1101 3331/1111
GCT GTC AGT GCA ATT CAC AGC CTG CTA AGT TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA
ala val ser ala ile his ser leu leu ser ser his asp leu asp pro arg cys val lys
3361/1121 3391/1131
CCA GAG GTG AAG GTC AAA ATC GCC GCC CTT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT
pro glu val lys val lys ile ala ala leu tyr leu pro leu val gly ile ile leu asp
3421/1141 3451/1151
GCT TTG CCA CAG CTC TGT GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC
ala leu pro gln leu cys asp phe thr val ala asp thr arg arg tyr arg thr ser gly
3481/1161 3511/1171
TCG GAT GAA GAA CAA GAA GGA GCC GGT GCC ATT AAC CAG AAT GTG GCT CTG GCC ATA GCA
ser asp glu glu gln glu gly ala gly ala ile asn gln asn val ala leu ala ile ala
3541/1181 3571/1191
GGG AAT AAT TTC AAT TTG AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG
gly asn asn phe asn leu lys thr ser gly ile val leu ser ser leu pro tyr lys gln
3601/1201 3631/1211
TAC AAC ATG CTG AAC GCG GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG
tyr asn met leu asn ala asp thr thr arg asn leu met ile cys phe leu trp ile met
3661/1221 3691/1231
AAA AAT GCT GAT CAG AGC CTC ATT AGG AAG TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC
lys asn ala asp gln ser leu ile arg lys trp ile ala asp leu pro ser thr gln leu
3721/1241 3751/1251
AAC AGG ATT TTA GAT CTA CTT TTC ATC TGT GTG TTA TGT TTT GAG TAT AAG GGA AAA CAG
asn arg ile leu asp leu leu phe ile cys val leu cys phe glu tyr lys gly lys gln
3781/1261 3811/1271
AGT TCT GAC AAA GTC AGT ACC CAA GTC CTG CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG
ser ser asp lys val ser thr gln val leu gln lys ser arg asp val lys ala arg leu
3841/1281 3871/1291
GAA GAG GCT TTG CTG CGT GGG GAA GGG GCC AGA GGG GAG ATG ATG CGC CGC CGG GCT CCA
glu glu ala leu leu arg gly glu gly ala arg gly glu met met arg arg arg ala pro
3901/1301 3931/1311
GGG AAC GAC CGA TTT CCA GGC CTA AAT GAA AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT
gly asn asp arg phe pro gly leu asn glu asn leu arg trp lys lys glu gln thr his
3961/1321 3991/1331
TGG CGG CAA GCT AAT GAG AAG CTA GAT AAA ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG
trp arg gln ala asn glu lys leu asp lys thr lys ala glu leu asp gln glu ala leu
4021/1341 4051/1351
ATC AGT GGC AAT CTG GCT ACA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT
ile ser gly asn leu ala thr glu ala his leu ile ile leu asp met gln glu asn ile
4081/1361 4111/1371
ATC CAG GCG AGC TCG GCT CTG GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG
ile gln ala ser ser ala leu asp cys lys asp ser leu leu gly gly val leu arg val
4141/1381 4171/1391
CTG GTG AAT TCT CTG AAC TGT GAT CAG AGT ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA
leu val asn ser leu asn cys asp gln ser thr thr tyr leu thr his cys phe ala thr
4201/1401 4231/1411
CTC CGT GCT CTC ATC GCC AAG TTT GGA GAC TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT
leu arg ala leu ile ala lys phe gly asp leu leu phe glu glu glu val glu gln cys
4261/1421 4291/1431
TTC GAC CTA TGT CAC CAA GTC CTG CAC CAC TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC
phe asp leu cys his gln val leu his his cys ser ser ser met asp val thr arg ser
4321/1441 4351/1451
CAA GCC TGT GCC ACC CTT TAC CTC CTC ATG AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT
gln ala cys ala thr leu tyr leu leu met arg phe ser phe gly ala thr ser asn phe
4381/1461 4411/1471
GCA AGA GTA AAG ATG CAA GTA ACC ATG TCC CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC
ala arg val lys met gln val thr met ser leu ala ser leu val gly arg ala pro asp

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FIG. 6
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4441/1481 4471/1491
TTT AAT GAA GAG CAC CTG AGA AGA TCC TTG AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC
phe asn glu glu his leu arg arg ser leu arg thr ile leu ala tyr ser glu glu asp
4501/1501 4531/1511
ACA GCC ATG CAG ATG ACT CCT TTT CCC ACC CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT
thr ala met gln met thr pro phe pro thr gln val glu glu leu leu cys asn leu asn
4561/1521 4591/1531
AGC ATC TTA TAT GAC ACA GTG AAA ATG AGG GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG
ser ile leu tyr asp thr val lys met arg glu phe gln glu asp pro glu met leu met
4621/1541 4651/1551
GAT CTC ATG TAC AGA ATT GCC AAG AGT TAC CAG GCA TCT CCT GAT CTG CGG CTG ACC TGG
asp leu met tyr arg ile ala lys ser tyr gln ala ser pro asp leu arg leu thr trp
4681/1561 4711/1571
CTC CAG AAC ATG GCA GAG AAA CAC ACC AAG AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC
leu gln asn met ala glu lys his thr lys lys lys cys tyr thr glu ala ala met cys
4741/1581 4771/1591
CTG GTG CAC GCC GCT GCG TTA GTG GCT GAG TAT CTG AGC ATG CTG GAG GAC CAC AGC TAC
leu val his ala ala ala leu val ala glu tyr leu ser met leu glu asp his ser tyr
4801/1601 4831/1611
CTG CCC GTG GGC AGT GTC AGC TTC CAG AAT ATT TCT TCC AAT GTG CTG GAG GAG TCT GTG
leu pro val gly ser val ser phe gln asn ile ser ser asn val leu glu glu ser val
4861/1621 4891/1631
GTC TCT GAG GAC ACC CTG TCA CCT GAC GAG GAT GGG GTG TGC GCA GGC CAG TAC TTC ACC
val ser glu asp thr leu ser pro asp glu asp gly val cys ala gly gln tyr phe thr
4921/1641 4951/1651
GAG AGT GGC CTG GTA GGC CTC CTG GAG CAG GCC GCG GAG CTC TTC AGC ACG GGA GGC TTA
glu ser gly leu val gly leu leu glu gln ala ala glu leu phe ser thr gly gly leu
4981/1661 5011/1671
TAT GAG ACA GTT AAT GAG GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA
tyr glu thr val asn glu val tyr lys leu val ile pro ile leu glu ala his arg glu
5041/1681 5071/1691
TTC CGG AAG CTG ACA CTC ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC
phe arg lys leu thr leu thr his ser lys leu gln arg ala phe asp ser ile val asn
5101/1701 5131/1711
AAG GAT CAT AAG AGA ATG TTT GGA ACC TAC TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT
lys asp his lys arg met phe gly thr tyr phe arg val gly phe phe gly ser lys phe
5161/1721 5191/1731
GGG GAT TTG GAT GAA CAG GAG TTT GTC TAC AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG
gly asp leu asp glu gln glu phe val tyr lys glu pro ala ile thr lys leu pro glu
5221/1741 5251/1751
ATC TCA CAT AGA CTA GAG GCA TTT TAT GGT CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG
ile ser his arg leu glu ala phe tyr gly gln cys phe gly ala glu phe val glu val
5281/1761 5311/1771
ATT AAA GAC TCC ACT CCT GTG GAC AAA ACC AAG TTG GAT CCT AAC AAG GCC TAC ATA CAG
ile lys asp ser thr pro val asp lys thr lys leu asp pro asn lys ala tyr ile gln
5341/1781 5371/1791
ATC ACT TTT GTG GAG CCC TAC TTT GAT GAG TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT
ile thr phe val glu pro tyr phe asp glu tyr glu met lys asp arg val thr tyr phe
5401/1801 5431/1811
GAG AAG AAT TTC AAC CTC CGG AGG TTC ATG TAC ACC ACC CCG TTC ACC CTG GAG GGG CGG
glu lys asn phe asn leu arg arg phe met tyr thr thr pro phe thr leu glu gly arg
5461/1821 5491/1831
CCT CGG GGA GAG CTG CAT GAG CAG TAC AGA AGG AAC ACA GTC CTG ACC ACT ATG CAC GCC
pro arg gly glu leu his glu gln tyr arg arg asn thr val leu thr thr met his ala
5521/1841 5551/1851
TTC CCC TAC ATC AAG ACC AGG ATC AGC GTC ATC CAG AAG GAG GAG TTT GTT TTG ACA CCG
phe pro tyr ile lys thr arg ile ser val ile gln lys glu glu phe val leu thr pro

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FIG. 6
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5581/1861                                   5611/1871
ATT GAA GTT GCC ATT GAA GAC ATG AAG AAG AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC
ile glu val ala ile glu asp met lys lys lys thr leu gln leu ala val ala ile asn
5641/1881                                   5671/1891
CAG GAG CCG CCT GAT GCA AAG ATG CTT CAG ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT
gln glu pro pro asp ala lys met leu gln met val leu gln gly ser val gly ala thr
5701/1901                                   5731/1911
GTA AAT CAG GGA CCA CTG GAA GTA GCC CAA GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA
val asn gln gly pro leu glu val ala gln val phe leu ala glu ile pro ala asp pro
5761/1921                                   5791/1931
AAA CTC TAT CGA CAT CAC AAC AAG TTG AGG TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT
lys leu tyr arg his his asn lys leu arg leu cys phe lys glu phe ile met arg cys
5821/1941                                   5851/1951
GGT GAA GCT GTA GAG AAA AAC AAG CGT CTC ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG
gly glu ala val glu lys asn lys arg leu ile thr ala asp gln arg glu tyr gln gln
5881/1961                                   5911/1971
GAA CTC AAA AAG AAC TAT AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA
glu leu lys lys asn tyr asn lys leu lys glu asn leu arg pro met ile glu arg lys
5941/1981                                   5971/1991
ATT CCA GAA CTG TAC AAG CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC
ile pro glu leu tyr lys pro ile phe arg val glu ser gln lys arg asp ser phe his
6001/2001                                   6031/2011
AGA TCT AGT TTC AGG AAA TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA
arg ser ser phe arg lys cys glu thr gln leu ser gln gly ser OCH

GAAAAGCCATCTTCATTCGTGGAGACTGTGGCCCTGCAACCCTGGAGAAGGACTTGCTGGTACTTAAAAAATGGGACATT
TGCCACCCAGGACTGACTGTACACTCCCTGATCAGCCAGCACTCTGGAAGCTTTGGGATCCCAGGAACCATGGAATTATT
CCCAAATGGACTCTGACCAGATTTTTGCCATACTGGGGGGTGGCGGGATGGAGGATGGGTACTCAGGCATGACTGCGTAT
TTATTAAAGTGTGTTTTTCCACAATGTACCAAACAAGGCATAAGCAGCTTCTCCTGCTGACTGGCCAATCACTGCCCATC
TGAGAGATGATTTCCTCTGGCCCATATTTGAATTTATTGGAGTAACTCAAATTGCCTGAGGAAAAATGGAAAAATTATCC
ACCAGTCGATTCAAACTGAATTTCACTCTTTATAGGAAGGCAGGGCAAACTTGTAGGAGTACGAAACATTTTCAATAAAT
CTACAAAGGGAAGCCTTACTACAATTCCAAAAATCATCATGGTTGGAAATTTGGGAGGAGATTATTTGTGAACTTGTTAC
CCTTTTGGTAATGGTGGACTAATTGCTGTATAGTTATTTTTGTTTTATTATTACTGTTACATTAATTTAACATGCATTTA
TAGAAGAATACATTCAAAGCACTGATGTAGGAGATACACGGTACTTGGAGCAGTCAGCCAAAAATCACAGATACTGCTTT
CACTTAAATGGAAACAATTCTCCGATAATGCTTTGCTTTTTTTCTTATGTCACTCTTGTGTACTATCTATTTTTCTCCTC
TCTGGGACCAAGTTTCTTTTTATAAAGCAATAATATCTCTGTTTTCATTTCAGAACATTGTGCTGTCTGTCAGCATATGT
ATATCAGCTACAAAATATATTCAACTTTGACTTCTTTTGACAAAGGACTTTAGGAAAAGGAGGAACAAAGACATTATTTG
AGAATTAAATTATATATTTTTAATATGACTGTGACCTTGACTGATAATAAAGATGTAATAAGAATTGCAAGCTAAAAAAA
AAAAAAAAAAAACTCG
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FIG. 6
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A. Allelic variations: single nucleotide changes (polymorphism) between CLASP-5 cDNA isoforms

Isoform	Nucleotide(s)	Consequence
1	1727	C to T change; mis-sense mutation changing codon from alanine to valine
2	1749	A to G change; silent mutation
3	2277	G to C change; silent mutation
4	2853	C to T change; silent mutation
5	3427	A to G change; mis-sense mutation changing codon from lysine to glutamic acid
6	3777	C to T change; silent mutation

B. Alternative splices

Isoform	Difference	Nucleotide(s)	Consequence
1	exon deletion	1806-1944	premature, in-frame stop codon leading to the production of a truncated, most likely soluble protein
2	exon insertion	between 2857 and 2858	additional, in-frame 48 nucleotide exon that contains a stop codon at the second codon, which would lead to a truncated, most likely soluble protein

These differences may be found separately or together in various combinations in the different human CLASP-5 isoforms

B

FIG. 6

nucleotide numbering
as in Figure 6A

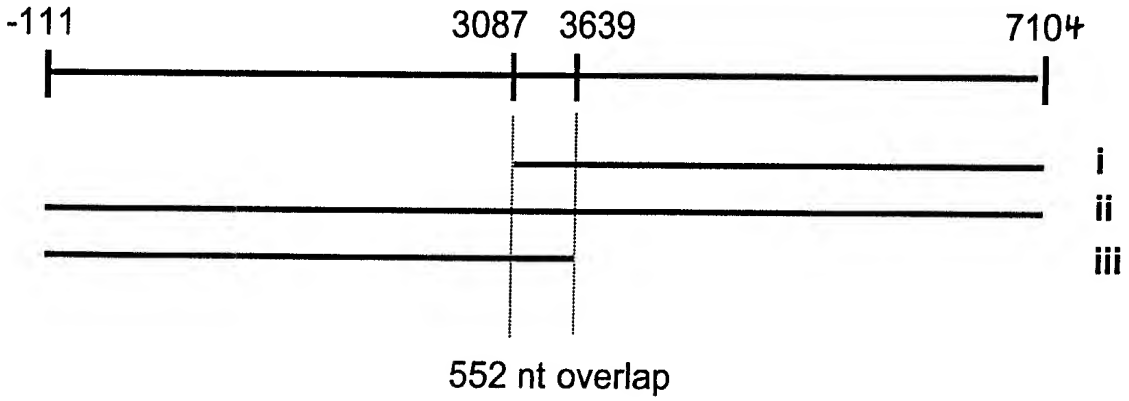

FIG. 6

1st partial exon (nucleotides 3793 to 3952)
CCAGCTGTCAGCCAAGCTCAGTAACCTTCCAACGCTCATTTCCATGAGGCTAG
AGTTCCTGAGAATCCTCTGTAGCCATGAGCATTACCTCAATCTGAACCTTTTT
TTTATGAATGCTGATACTGCTCCAACATCTCCTTGTCCTTCCATATCTTCCCAG
GTAATAAAAGAATTATTTAACTAAAAGAATTATTCAAGCTAT

2nd exon (nucleotides 5809 to 5948)
GCTCATAAAATGGCTCCTTACGTTTCTGTAGAACTCAAGCTCCTGCTCCAGCT
TCCAGGACCAGAAGATCGCCAGCATGTTCGATCTGACTTCCGAGTACCGCCA
GCAGCACTTCCTCACCGGGCTCCTCTTCACAGAACTGGCTGCTGCCCTGGATG
CCGAAGGGGAAGGGTATGTTTCTGGCATTTAAAATGGAAGATGAAGC

3rd exon (nucleotides 13662 to 13831)
CATAACCTCTTGATTCCTGTGTTGTGCCAACAGAATCAGCAAAGTACAAAGG
AAAGCTGTCAGTGCAATTCACAGCCTGCTAAGTTCTCACGACCTGGACCCAC
GCTGTGTCAAACCAGAGGTGAAGGTCAAAATCGCCGCCCTTTACCTACCTTTA
GTTGGCATCATTTTGGATGCTTTGCCACAGCTCTGTGACTTTACAGGTAATGG
CCCTTCTGTTTTCTTTCTTGGATTG

4th exon (nucleotides 16948 to 17087)
TGTTTGACTTGACATCACAAACGATGTTTTCATTGCAGTTGCAGATACTCGCA
GATACCGCACCAGTGGCTCGGATGAAGAACAAGAAGGAGCCGGTGCCATTA
ACCAGAATGTGGCTCTGGCCATAGCAGGGAATAATTTCAATTTGAAAACAAG
TGGAATAGTGCTGTCTTCCTTGGTATGTTGGTGCACATGTGTCTGGTTGATTTT
TCAT

5th exon (nucleotides 19281 to 19463)
TGGCCTCCATCCCCCAATCTGCCTCCCTTCAGCCCTATAAGCAGTACAACATG
CTGAACGCGGACACTACTCGCAACCTCATGATCTGCTTCCTCTGGATCATGAA
AAATGCTGATCAGAGCCTCATTAGGAAGTGGATTGCTGACCTGCCATCAACG
CAGCTCAACAGGATTTTAGATCTACTTTTCATCTGTGTGTTATGTTTTGAGTAT
AAGGTAAGTCTGGAGTGGCACAACTTTATACCAGC

6th exon (nucleotides 19829 to 19958)
CACCAAAGGACATGTCCTCCTACCTCTGTCTTGTCCAGGGAAAACAGAGTTCT
GACAAAGTCAGTACCCAAGTCCTGCAGAAGTCAAGGGATGTCAAGGCCCGG
CTGGAAGAGGCTTTGCTGCGTGGGGAAGGGGCCAGAGGGGAGATGATGCGC
CGCCGGGCTCCAGGTGTGTTGGACTGGCCCTTCCCTGCTCTCTGTCAAGC

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FIG. 7
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7th exon (nucleotides 20928 to 21015)
TCAAATTCCTATCATGCATTTCTTAACTCCTAGGGAACGACCGATTTCCAGGC
CTAAATGAAAATTTGAGATGGAAGAAAGAGCAGACACATTGGCGGCAAGCT
AATGAGAAGCTAGATAAGTGAGTCACTCGGCAACTTTCTGCTACTTTTACCT

8th exon (nucleotides 25765 to 25861)
GCTTTAATTTGACCTCTTGTTGTTTCCTAGAACAAAGGCCGAGTTAGATCAAG
AAGCCTTGATCAGTGGCAATCTGGCTACAGAAGCACATTTAATCATCCTGGA
TATGCAGGAAAACATTATCCAGGTGAGGAAAACAAACACCCAATCTGATTTG

9th exon (nucleotides 27242 to 27376)
GGATTCAATGATGCTGTTCTTCCATTCCCCCAGGCGAGCTCGGCTCTGGACTG
TAAAGACAGCCTGCTGGGAGGTGTTCTGAGGGTGCTGGTGAATTCTCTGAAC
TGTGATCAGAGTACCACCTACCTGACTCACTGCTTTGCAACACTCCGTGCTCT
CATCGCCAAGGTAAACTTGGGATGCTTGTTTTCTTCCTCTTAATT

10th exon (nucleotides 28582 to 28734)
AGTGATGCCTAATGGCCCTTTATGTCTCTCCTAGTTTGGAGACTTACTCTTCG
AAGAGGAGGTGGAACAGTGTTTCGACCTATGTCACCAAGTCCTGCACCACTG
CAGCAGCAGCATGGATGTCACCCGGAGCCAAGCCTGTGCCACCCTTTACCTC
CTCATGAGGTTCAGTTTTGGAGCCACCAGTGTAAGAGTTCAAACCAGCTGAG
TGACCTGGAATCAG

11th exon (nucleotides 31046 to 31204)
TTACTTCATCTTTTTTTTTTTTTCACTGATGCAGAATTTTGCAAGAGTAAAGA
TGCAAGTAACCATGTCCCTGGCATCTTTGGTGGGAAGAGCACCAGACTTTAA
TGAAGAGCACCTGAGAAGATCCTTGAGGACAATTTTGGCCTATTCAGAAGAG
GACACAGCCATGCAGATGACTCCTTTTCCCACCCAGGTACACCGAAGCACAT
ACCTTGTCTCATGCATGAGT

12th exon (nucleotides 32755 to 32855)
AGCTAAGATTATTTTGAGGCTTACACTTTTTGCAGGTGGAGGAACTTCTCTGT
AATCTGAATAGCATCTTATATGACACAGTGAAAATGAGGGAATTTCAGGAAG
ATCCTGAGATGCTTATGGATCTCATGTACAGGTAAGCTTTCCTGACACACTCA
AGGGACACCATTT

13th exon (nucleotides 33663 to 33855)
TCCTCAAAACTACTTCTCACTCAATCTGTCTTCAGAATTGCCAAGAGTTACCA
GGCATCTCCTGATCTGCGGCTGACCTGGCTCCAGAACATGGCAGAGAAACAC
ACCAAGAAGAAGTGCTACACGGAGGCTGCCATGTGCCTGGTGCACGCCGCTG
CGTTAGTGGCTGAGTATCTGAGCATGCTGGAGGACCACAGCTACCTGCCCGT
GGGCAGTGTCAGCTTCCAGGTAGGGTGTGTGCAGCTTTTCCCTTAGAGCAGTG
GTTC

14th exon (nucleotides 38125 to 38268)

CTGTTCTCCAGGCTTATACTGTGGTCTCTTTCAGAATATTTCTTCCAATGTGCT
GGAGGAGTCTGTGGTCTCTGAGGACACCCTGTCACCTGACGAGGATGGGGTG
TGCGCAGGCCAGTACTTCACCGAGAGTGGCCTGGTAGGCCTCCTGGAGCAGG
CCGCGGAGCTCTTCAGCACGGTCAGTGCCCAGAGGGCATCCCGGGGCCTGGC
C

15th exon (nucleotides 40166 to 40297)
AATTCTCTCTGATGCTCTTCTCCTCTTTCCAAGGGAGGCTTATATGAGACAGT
TAATGAGGTCTACAAGCTGGTCATCCCCATCCTAGAAGCGCATCGAGAATTC
CGGAAGCTGACACTCACTCACAGCAAGCTGCAGAGAGCCTTCGACAGCATCG
TTAACAAGGTAGCCGGGGAGCCTGGCTGGCAGGTCTTGTTAC

16th exon (nucleotides 40755 to 40889)
TAAGGAGAGCTTTTTATATTTTGTTCCTCAGGATCATAAGAGAATGTTTGGAA
CCTACTTCCGAGTTGGTTTCTTTGGATCCAAATTTGGGGATTTGGATGAACAG
GAGTTTGTCTACAAAGAGCCTGCAATTACCAAGCTTCCTGAGATCTCACATAG
ACTAGAGGTAAGAAAAGTGATTCTGTGCGCCTGACCTGGTACACTTTAC

17th exon (nucleotides 42307 to 42396)
AACCTTTATAAACTGTTGGTTCTTCTTACCTAGGCATTTTATGGTCAATGTTTT
GGTGCAGAATTTGTGGAAGTGATTAAAGACTCCACTCCTGTGGACAAAACCA
AGTTGGATCCTAACAAGGTATACAAAAATTTACAAAAACTAACCATCAAGC

18th exon (nucleotides 45250 to 45486)
TCTTCTCCCTCCGTGCCTTTTCCCCCTTAGGCCTACATACAGATCACTTTTGTG
GAGCCCTACTTTGATGAGTATGAGATGAAAGACAGGGTCACATACTTTGAGA
AGAATTTCAACCTCCGGAGGTTCATGTACACCACCCCGTTCACCCTGGAGGG
GCGGCCTCGGGGAGAGCTGCATGAGCAGTACAGAAGGAACACAGTCCTGAC
CACTATGCACGCCTTCCCCTACATCAAGACCAGGATCAGCGTCATCCAGAAG
GAGGAGGTAATGCACCCAAGGGATTGGCCACCACTGGATGAGT

19th exon (nucleotides 48664 to 48807)
ACAGTGACTTCCCTATGTTTACGTCTCATGTTCAGTTTGTTTTGACACCGATTG
AAGTTGCCATTGAAGACATGAAGAAGAAGACCCTGCAGTTAGCAGTTGCCAT
TAACCAGGAGCCGCCTGATGCAAAGATGCTTCAGATGGTGCTGCAAGGCTCT
GTGGGAGCTACTGTAAATCAGGTAAGCAAAACCAGAGGTGGCAGCTCCT

20th exon (nucleotides50892 to 50998)
TATATTCTTTTTTTTTTTTTTTTTTTTTTCCCACCAGGGACCACTGGAAGTAGC
CCAAGTGTTTTTGGCTGAAATTCCTGCTGATCCAAAACTCTATCGACATCACA
ACAAGTTGAGGTTATGCTTTAAGGAATTCATCATGAGGTAAGAAGGAAAATG
GCTGGGAATTTCAGTAGAG

21st exon (nucleotides 62398 to 62568)
TCATTTATTTCTCCCACACTGATATTTTCATCTCAGATGTGGTGAAGCTGTAG
AGAAAAACAAGCGTCTCATCACGGCAGACCAGAGGGAATATCAGCAGGAAC

TCAAAAAGAACTATAACAAGCTAAAAGAGAACCTCAGGCCAATGATCGAGC
GGAAAATTCCAGAACTGTACAAGCCAATATTCAGAGTTGAGAGTCAAAAGAG
GTAAGAACAGGGCAGAGGAGGCCTCTTCCTGTGGGAT

22nd exon (nucleotides 63040 to 63294)
CCTCCCTCTCTTTTCTTAATTTCAGGGACTCCTTCCACAGATCTAGTTTCAGGA
AATGTGAAACCCAGTTGTCACAGGGCAGCTAAGAAAAGCCATCTTCATTCGT
GGAGACTGTGGCCCTGCAACCCTGGAGAAGGACTTGCTGGTACTTAAAAAAT
GGGACATTTGCCACCCAGGACTGACTGTACACTCCCTGATCAGCCAGCACTC
TGGAAGCTTTGGGATCCCAGGAACCATGGAATTATTCCCAAATGGACTCTGA
CCAGATTTTTGCCATACTGGGGGGTGGCGGGATGGAGGATGGGTACTCAGGC
ATGACTGCGTATTTATTAAAGTGTGTTTTTCCACAATGTACCAAACAAGGCAT
AAGCAGCTTCTCCTGCTGACTGGCCAATCACTGCCCATCTGAGAGATGATTTC
CTCTGGCCCATATTTGAATTTATTGGAGTAACTCAAATTGCCTGAGGAAAAAT
GGAAAAATTATCCACCAGTCGATTCAAACTGAATTTCACTCTTTATAGGAAG
GCAGGGCAAACTTGTAGGAGTACGAAACATTTTCAATAAATCTACAAAGGGA
AGCCTTACTACAATTCCAAAAATCATCATGGTTGGAAATTTGGGAGGAGATT
ATTTGTGAACTTGTTACCCTTTTGGTAATGGTGGACTAATTGCTGTATAGTTAT
TTTTGTTTTATTATTACTGTTACATTAATTTAACATGCATTTATAGAAGAATAC
ATTCAAAGCACTGATGTAGGAGATACACGGTACTTGGAGCAGTCAGCCAAAA
ATCACAGATACTGCTTTCACTTAAATGGAAACAATTCTCCGATAATGCTTTGC
TTTTTTTCTTATGTCACTCTTGTGTACTATCTATTTTTCTCCTCTCTGGGACCAA
GTTTCTTTTTATAAAGCAATAATATCTCTGTTTTCATTTCAGAACATTGTGCTG
TCTGTCAGCATATGTATATCAGCTACAAAATATATTCAACTTTGACTTCTTTTG
ACAAAGGACTTTAGGAAAAGGAGGAACAAAGACATTATTTGAGAATTAAATT
ATATATTTTTAATATGACTGTGACCTTGACTGATAATAAAGATGTAATAAGAA
TTGCAAGCTAAAAAAAAAAAAAAAAAAAA

FIG. 7

A

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1       GTTCTCTGTGGTTAGTCACTTAGTGACTTTAGATAAGTTTTTCCAATTTTATGGGTCTTAATTTCCTCAGTTTTAAAATAAGAAGGGGGGG
92      TTGAGAGATTTGAGGGCTGATCAACGAAAAGGATAGGACCATAAAAAAGCAGTGACATACAAGCTTCATTGAGCAGCACTTGGACAGGGTTA
183     CATAAGAGCGGAAGCCCCTCCCAGCATGAGAACAGCCATAGGCCTGCAGTGAGGAGGGGACCATCCAGAGGAGCAGGGGAACTCCCAGGGG
274     AGAGGAGGATTAGGGCAGAAGCTTATAGATCTGGGTGAGGCTGCTCCACAGCACAGTAGGGAGTCTCTGGGTCAGAGAGCTCCAAGGGCTG
365     TAGCAGCTTAGGGCCCTGTATCTGCAAGGCTCTATCTTATCATTAGGAAACAGCTGTCCATCGAGATTTTATGGGGTCTGCAAAGGAGGCA
456     GGCACTAAATGGATGAAAATCTGCTTATATGAGCTATTTTTGTTAATGACTGGGCATGGTAAAATTTGAGTTAGGTATGAGCCAAGGGATC
547     AGCACCAGTCGACAGTGAAGAAATAAACAACCGAGGGGCCAATACACAGAAACAATCTTTGACTTGTTTACATAACACCTCTCCTCCAAAA
638     AAAGAAAAAGACATGACTTTTCTAAAGGAAGTCCTGTCTACAGCCATACCACCCTGAACGCACGCAGTCTCATCTAAGGGAAGTCCTGATA
729     AGGAAGCAGAATAATAAAAAAGAATCCTAAGGAAACATCAGAAGTCCCCAAGCATCCCCATCCCATGCACCCTGACCCCTGCCCTGCAGCG
820     GATCTTCTGTCCCAGGACCCACCAGAATAGAATGGCAGAGGGACACTTCACTCCTCCTTGCCCTCCCTCTTCAGTATTTAGGATTCCAGGT
911     TAGTCTGTTTTCAAAACTTTAAGTTGAGTGTATGAAAGATACCCTAGATCACCACTGCAGACCCAGGCTTAGCTACTCACATGCAGGCTAT
1002    CTTCATTCCCGACAGGGAAATAAGGCAACCCAAGGTAGATATCTGCCTTCCCTGCAAAACTCATGTTTTTATTTTCTCTTTCTCTTTCCTT
1093    TCTTTTCTCTTGCTCACTATCTTTCTCCTTAAATTCTTCCCTTTTCTTTTAGTTACCATTTCTTTTTTTGTTTCTCTCCTTGACTCAAATG
1184    CCAAAGATCCCTAGACCAGGAGTCAAGAAGCCTGCATGCTGATTCCTGGGACACCATTAATTACTTCTGTGATTGGGAGCATCAGCCTTTG
1275    AGGCATTCATTTCCTCATCTGCAAAAAAACTAGGCTGGATTAGATTTATCCACTGATTCTGTGGTCTGTGTCTGCCAGTGACATCCACGGA
1366    TGTTACTTAGCACCATTAGTGGCACTCAGGCCTCAGAAGGTCACTGACCCCCATTCGTGGTGATTTAATTCATTGATCCCAGCTCTCTAGA
1457    TACAGGATGAACTTCATACCTTAAGCAAGTTGTATTCTTACAAAGTCGTCTGACTTTATCATTTTGCATAACCTATTATGTTTTCTGCCAT
1548    CTAAAGATTTTGTGGCAATGGATATAACCTTAGTCTTTTTTAATAGTCACTAAAAATAGACAAATCCATTTCCTCAATTACTGTCTGTCAC
1639    TTACAATGTGCCACTAAGCAAACACCCATCCCTTGGGTAGGGGCATTGTGGGTCTTGACCTTTGGGAAGGAAGTTTTTGGAATGCACCTTA
1730    CTCCTCTTTTCAAAACATCACTCAAATTGTTTTTGAAATGTCTATTTTTTTTCTTTTGAGATGGAGTCTTACTCTGTTGCCCAGGCCAGAG
1821    TGCAGTGGCACAATTTTGGCTCACTGCAAACTCCGCCTCACAGGTTCAAGCGATTCTCCTTCCTCACCCTCCCGAGTAGCTGGGATTACAG
1912    GTGTGTGGCACCACTCCCCGCTAATTTTTGCATTTTTAGTAGAGACAGGGTTTCACCATGTTGGCCAGACTGGTCTTGAACTCTGGCCTCA
2003    AGTGATCTGCCTGCCTCTGCCTCCCGAAGTGCTGGGATTACAGGTGTGAGCCACCACACCCAGCCTGAAATGTCTGTCTTGAATGATGTCT
2094    CAAGGGACCTATGAAAGATACCCATAGTGGGGCCTTCTTTTAAGTGCCAATGTGTTGTGGGTTCAAGTTCCGATAGCCGGCTTGACCCGAC
2185    ACCTGTTAATGAGTAACCTAAGTGACAGGCACATGACCAAGTTCTAATCCCTTCAATGTGCTGGTGGCTCCACTGGTCCAAAGTCAGCCAG
2276    GAGTGCACATCGAAAGGTTATGGGATCTGGTAACTGTGCTTACATAGAAGTCATATGTTTTGGTTTTAAAATAATATATAATGGCATTTAC
2367    TTATTTTAAGTGGATGTCTAACTATGAATTAATTCTGTAGGCAATATGTCCCACAACACATTGGCTTCTTGTAAAATGGCTGAAAATATGT
2458    GTTCATTTAAATTATATTGTTTAGTCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGGAGGATCACCTGAGGCCAGGAGTTCGAGACCAG
2549    CTTGGCCAATATGGTTAAACCCCATCTCTACTAAAAATACAAAAAATTAGCTGGGCATGTTGATGTGCACCTGTAATCCCAGCTACTCGGG
2640    AGGCTGAGGCAAGAGAATCGCTTGAACCTGGGAGATGAAGGTTGCAGTGAGCCGAGATCATGCCACTGCACTCCAGTTCAACAGAGCAAGA
2731    CTCTGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTATATATATATATATATATATATACATATATATATATGTGTATATATATA
2822    TGTGTATATATATATATGTATATATATATATATGTGTATATATATATATGTGTATATATATATATATATAGTTTAAAAAACAAACTACTCT
2913    TGAAGTGAGTGAAGAGGAGGCATGTCTATCACAAGGATGATGCTTCATATTTCTGTGCTGGGGTGGGGGGTGATAATGATGAAATATTGAG
3004    GAGCTCAAGGTGCATCAGCGCCCCTTCCTTCCCCTATTTTGCCTTTAGAGGAGCTGCCTCTGAGTCTGGGTCTTTCAGTTGTTCAGCTTGC
3095    CTGGGGGAAGCAAGGGGTCTCTTCCAGACAGTCACCTTTTTCTGCTTTTCATTGCTTGCTTCATGGTTTATTTTTTAAAGGAAGATTTTTC
3186    CTAAAAACTCTTCTAGCTTTCTTTCTCTTTCTTCTCCATTTCCTCCTCTCTCAGTCTGGGACAAGCTCCTTGAGTTTTTTGCAGGTACTAT
3277    GTACTTTGCTAAACAGTTTGATGCCTTTCTCTAGGGAACTGGTTCTACAACTTTCCAATGGGGCCTTTAATTAGAAACTACGAGAGAACAC
3368    TTGTAGTATAAAAGTCATCTAGTCATATTCTATTAGTTTCATACAGGCTCATATGAGGTCAACTCCTTTCATTTAGTTTCTCGAACATAGT
3459    AGAGTTTTTGTAAAATTAATTATGTTACGGTGAAGATGTACCTCAAGATTTTCAGCACAGGCTTCCCATGGTATTAAAGATTTGATAAAGT
3550    GGAAATCGGGATAAGAATCCTCATTCTGGACAGCTACTAGGCTAGAATCACTAAGGGGAACAGTAATGAATGAAAATTTATTAGACCTCTC
3641    TGTAATGCAGAATTTACCATCTGTTGCACTATCCCATTAGTTTTTATTAAATTGATTGCCTTAACCTGGAGAGAAAGGATATTTTTGTGTC
3732    TGCCAACCTCAACTCCACTTACCTTGTAATAAATGTTTCATTCCTCTTTTCATTTTTCTTCCCAGCTGTCAGCCAAGCTCAGTAACCTTCC
3823    AACGCTCATTTCCATGAGGCTAGAGTTCCTGAGAATCCTCTGTAGCCATGAGCATTACCTCAATCTGAACCTTTTTTTTATGAATGCTGAT
3914    ACTGCTCCAACATCTCCTTGTCCTTCCATATCTTCCCAGGTAATAAAAGAATTATTTAACTAAAAGAATTATTCAAGCTATTTCATTTAAC
4005    TAGCTCAGTTTAATCATGTATTTCCTATAAAGGTTAGTCTTATTAATTTGACAAAAAATCAAACAATTCAAACCAGATCAAGTATGCTACC
4096    CTGAAGTTACACCACTAGCTAAGAATTAACAATCTAAGTAATTGGTTTCTCCCCAGGCTCAAGGCTCCCTGATCAGGTTAAGTAAAGCCAA
4187    GAATCCAATAAGCCCTATGAAATTTAGAAACTCATAGAAAAGTCTCAAATCTTCCTTTGTCTGACATTAGCCAATTGTTATATTATGCAAA
4278    TAGAGGATTCCAAAGTAAATAAGTTTTGGAAACCATGTATTCACCAGGTTTCTTTGCAGCAGGCCCTCTAAGAGGTTTTAACTTGTTCATG
4369    TCAATTGCAAATGCACGAGAAGCAGAAGAGGAAATGGGAGGAGGTGTGCATGATAAGCAGTGATTCCCCAAATGATTTAACATGGAAACCC
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FIG. 7
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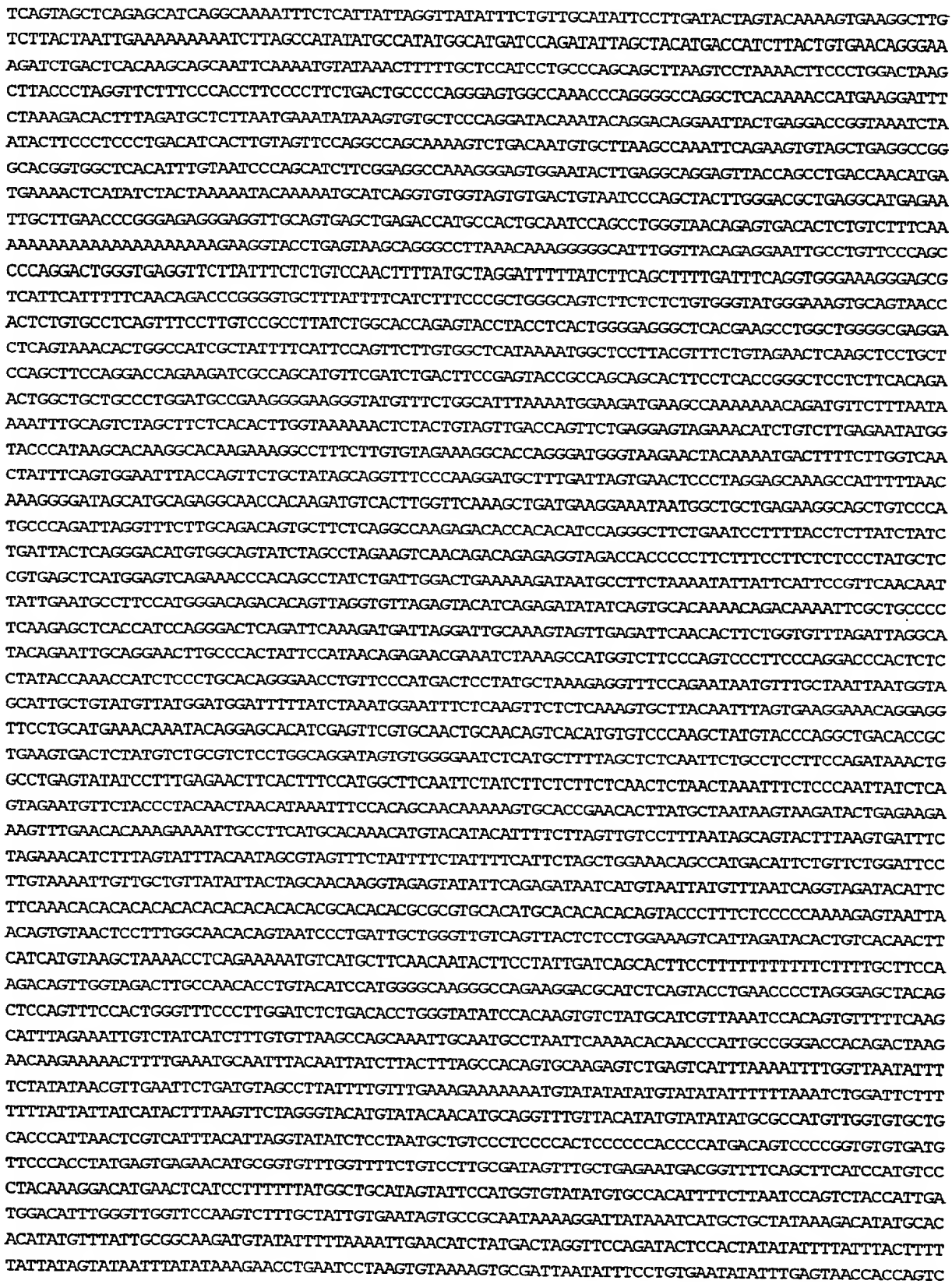
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4733 AGATCTGACTCACAAGCAGCAATTCAAAATGTATAAACTTTTTGCTCCATCCTGCCCAGCAGCTTAAGTCCTAAAACTTCCCTGGACTAAG
4824 CTTACCCTAGGTTCTTTCCCACCTTCCCCTTCTGACTGCCCCAGGGAGTGGCCAAACCCAGGGGCCAGGCTCACAAAACCATGAAGGATTT
4915 CTAAAGACACTTTAGATGCTCTTAATGAAATATAAAGTGTGCTCCCAGGATACAAATACAGGACAGGAATTACTGAGGACCGGTAAATCTA
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5188 TGAAAACTCATATCTACTAAAAATACAAAAATGCATCAGGTGTGGTAGTGTGACTGTAATCCCAGCTACTTGGGACGCTGAGGCATGAGAA
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5370 AAAAAAAAAAAAAAAAAAAAGAAGGTACCTGAGTAAGCAGGGCCTTAAACAAAGGGGGCATTTGGTTACAGAGGAATTGCCTGTTCCCAGC
5461 CCCAGGACTGGGTGAGGTTCTTATTTCTCTGTCCAACTTTTATGCTAGGATTTTTATCTTCAGCTTTTGATTTCAGGTGGGAAAGGGAGCG
5552 TCATTCATTTTTCAACAGACCCGGGGTGCTTTATTTTCATCTTTCCCGCTGGGCAGTCTTCTCTCTGTGGGTATGGGAAAGTGCAGTAACC
5643 ACTCTGTGCCTCAGTTTCCTTGTCCGCCTTATCTGGCACCAGAGTACCTACCTCACTGGGGAGGGCTCACGAAGCCTGGCTGGGGCGAGGA
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5825 CCAGCTTCCAGGACCAGAAGATCGCCAGCATGTTCGATCTGACTTCCGAGTACCGCCAGCAGCACTTCCTCACCGGGCTCCTCTTCACAGA
5916 ACTGGCTGCTGCCCTGGATGCCGAAGGGGAAGGGTATGTTTCTGGCATTTAAAATGGAAGATGAAGCCAAAAAAACAGATGTTCTTTAATA
6007 AAATTTGCAGTCTAGCTTCTCACACTTGGTAAAAAACTCTACTGTAGTTGACCAGTTCTGAGGAGTAGAAACATCTGTCTTGAGAATATGG
6098 TACCCATAAGCACAAGGCACAAGAAAGGCCTTTCTTGTGTAGAAAGGCACCAGGGATGGGTAAGAACTACAAAATGACTTTTCTTGGTCAA
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6371 TGCCCAGATTAGGTTTCTTGCAGACAGTGCTTCTCAGGCCAAGAGACACCACACATCCAGGGCTTCTGAATCCTTTTACCTCTTATCTATC
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6553 CGTGAGCTCATGGAGTCAGAAACCCACAGCCTATCTGATTGGACTGAAAAAGATAATGCCTTCTAAAATATTATTCATTCCGTTCAACAAT
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6735 TCAAGAGCTCACCATCCAGGGACTCAGATTCAAAGATGATTAGGATTGCAAAGTAGTTGAGATTCAACACTTCTGGTGTTTAGATTAGGCA
6826 TACAGAATTGCAGGAACTTGCCCACTATTCCATAACAGAGAACGAAATCTAAAGCCATGGTCTTCCCAGTCCCTTCCCAGGACCCACTCTC
6917 CTATACCAAACCATCTCCCTGCACAGGGAACCTGTTCCCATGACTCCTATGCTAAAGAGGTTTCCAGAATAATGTTTGCTAATTAATGGTA
7008 GCATTGCTGTATGTTATGGATGGATTTTTATCTAAATGGAATTTCTCAAGTTCTCTCAAAGTGCTTACAATTTAGTGAAGGAAACAGGAGG
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7281 GCCTGAGTATATCCTTTGAGAACTTCACTTTCCATGGCTTCAATTCTATCTTCTCTTCTCAACTCTAACTAAATTTCTCCCAATTATCTCA
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8009 AGACAGTTGGTAGACTTGCCAACACCTGTACATCCATGGGGCAAGGGCCAGAAGGACGCATCTCAGTACCTGAACCCCTAGGGAGCTACAG
8100 CTCCAGTTTCCACTGGGTTTCCCTTGGATCTCTGACACCTGGGTATATCCACAAGTGTCTATGCATCGTTAAATCCACAGTGTTTTTCAAG
8191 CATTTAGAAATTGTCTATCATCTTTGTGTTAAGCCAGCAAATTGCAATGCCTAATTCAAAACACAACCCATTGCCGGGACCACAGACTAAG
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8373 TCTATATAACGTTGAATTCTGATGTAGCCTTATTTTGTTTGAAAGAAAAAAATGTATATATATGTATATATTTTTTAAATCTGGATTCTTT
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8919 ACATATGTTTATTGCGGCAAGATGTATATTTTTAAAATTGAACATCTATGACTAGGTTCCAGATACTCCACTATATATTTTATTTACTTTT
9010 TATTATAGTATAATTTATATAAAGAACCTGAATCCTAAGTGTAAAAGTGCGATTAATATTTCCTGTGAATATATTTGAGTAACCACCAGTC

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FIG. 7
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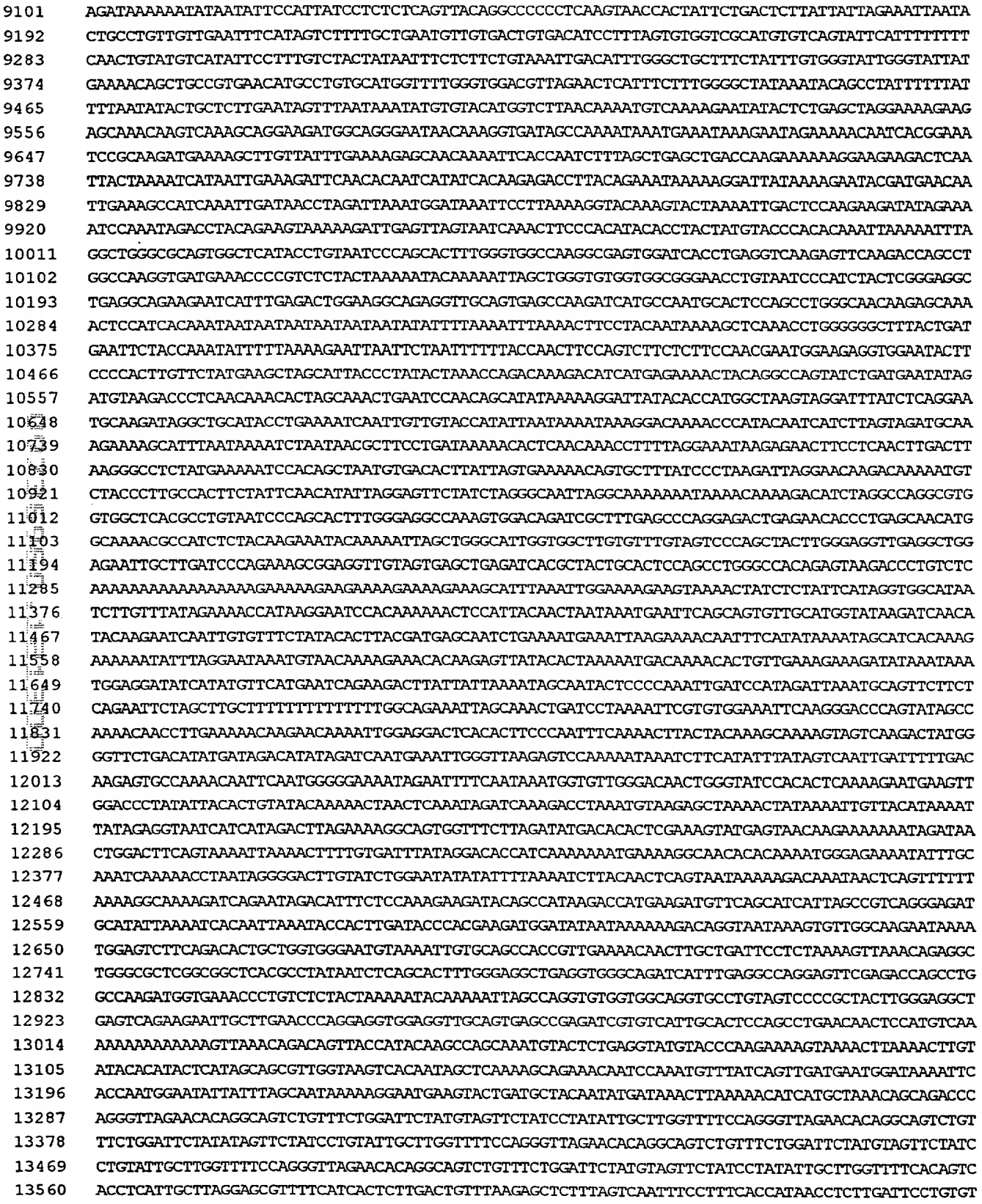
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FIG. 7
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15744 CCCTATGGCAATTAAGGGGAAATAAGAATGTGTCTCTATGTTAGTTGTGATAATGTTATCAGGTCTTGCATAATTTCCATGTGCTGTTTAT
15835 TTAACCATTTGTTTAAAATCCCAATGGCCTTAATAAGTATTTCTAAAAATTGGGTTTTGGCTCGGTGTGGTGGCTCACCCCTGTAATCCCA
15926 GCACTTTGGGAGGCCAAGGTGGACAGATCACTTGAGGCCAGGGGTTCAAGACCAGCCTGGCCAACATGGCGAAACCCTGTCTCCACTAAAA
16017 ATACAAAAGTTAGCCAGGCGTGGTGGCGCACCTGTAATCCCAGCTACTCGGGAGGCTGAGGTAGGAGGATGGAGGGGCAGAGATTGCAGTG
16108 AGCGGAGATGGCGCCACTGCACTCCAGCCTGGATGATAGTGTGAGACTTTGTCTAAAAATAAATAAATAAATAAATAATAAGAACTGGGTT
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16290 TAGAAAAACATGAATTTTTAGGAAAACATGAGTGAATCAATCAGTTGTGAATGTTTTACCACACTTTTCCCAGAACTGCTTGAAATATTAA
16381 TAGTTTTTGATTGTATACTGGTAGCATTCTTAAAAACCAGACTTTTAAACGGTTTATCGTTTTTTTGCTTGCATACATCTAGACCTATCTA
16472 TAAATATGGGTATGTCTATATTACATAGATACAATAAATTGACATTCATTTTAAACATTTGAAATATGACAAATTATTGCTGAACTTGTGA
16563 TAATAGCTTATTATTCTATATAAGGTAGTTGCTTAATTCTGTAATTGTAGGTGTCTTCTATTTGGTCATTATTTAAAATAATGCCAATTAT
16654 TAGAATAGAGAATGAAGTTTAAAAAATTATGTTACAGGAAACAATTATGGAAGGTTTGAAAACTTTTTGTTCACACAATTTGAAAAATTAA
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16836 TGAAATTACTGTGCTGACTTTAGTGACTGAGAAGTATCAGTCTCTTATTGGGTAGGGGACATGGGGAAATGTCATGTTTGACTTGACATCA
16927 CAAACGATGTTTTCATTGCAGTTGCAGATACTCGCAGATACCGCACCAGTGGCTCGGATGAAGAACAAGAAGGAGCCGGTGCCATTAACCA
17018 GAATGTGGCTCTGGCCATAGCAGGGAATAATTTCAATTTGAAAACAAGTGGAATAGTGCTGTCTTCCTTGGTATGTTGGTGCACATGTGTC
17109 TGGTTGATTTTTCATTTCATGTCTTCTGTCTTCTGTTTTGTTTTGTTTGTTTGTTTTGAGACAGAGTCTCACTCTGTTGCACAGGCT
17200 GGAGTGCAGTGGCGCAATCTCAGTTCACTGCAACCTCCGCCTCCCGGGTTCTTCATGCCTCAGCCTCCTGATTAGCTGGGATTACAGGCGT
17291 GCACCACCACACCTGGCTAATTTTTTTTTGTATCTTTTAGTAGAGACGGGGTTTCGCCATGTTGGCCAGGCTGGTCTCAAACTCCCAACCTC
17382 AGATGGTACACCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGTGCCCAGCCTCTTCTGTCATCTTCTGATGGGAGA
17473 ACTCAGCTTAGAGCAGGCATTGATTATTTCCGCCTCATTTTGCTGGAAAGAATCATTGTGAGGCTGGCAGCTGAGGTGCACACAAGTCAGA
17564 AAGGGTTCTGGCAACAGCAAGAGATGTGCAGATCAAATTCAGGCAGTCCCAGTGGTGCTGAGTTCAAGTTCAAGAAACCGGAAAAGAGGAA
17655 AACTTGGGAAATCTGAAATCCTTGCAAAGGAGATCAAACCAAGGCTCTCTGAGGGTGGAGGCTTAGGCTGTGTTCAGTCTATGTGTGTGTA
17746 ATTCATACAGTGTAATGCCTCCAAAAAAAAAGACTGAAGGAGGCTGGTAGCTTAGCGTAAGGGCTTCTTAAACAAGACTGCAGCTTTTCTA
17837 GGACCCCAGGGAGCCTAAGGAGGGTTGTTTGGCTCTGTCCTTTTGCATGGACTCTGTGGGCTCAAAGAGGGGCTCCTCTGGGAATGTATCC
17928 TCTGATTCAGTTGAGGTGGGATTCATCTCTGTTCATTGATGAGCTCTGACTATCCCTTGTGAAGACAGCACTGCATCCTCCAATGTCATTT
18019 ACTTTCACATTTCAATGTAGGGTATAGATGTGCAGAGAATTTAACTTTCTTCTCCCGTGAGAAAGCAGCATCCTGACCTAACTCTTCTTGC
18110 TGGATGACTTTCTTGTCTTCCTTCCTGCACTTAGCAAGCTCCATCACCATGAGGATTGGGGGGACAGTGAGGCAGGAAGATGAGACAGAGA

FIG. 7
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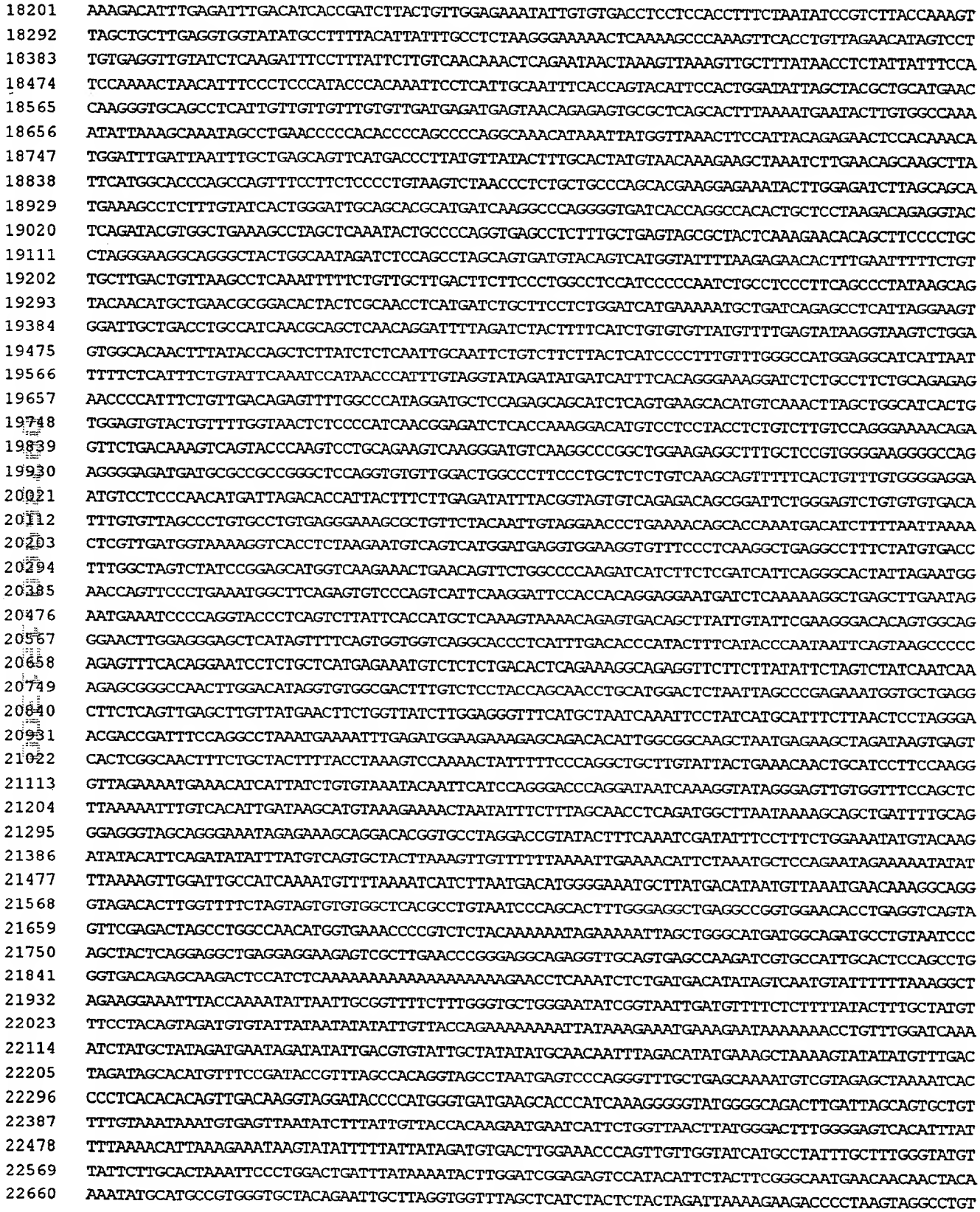
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18383 TGTGAGGTTGTATCTCAAGATTTCCTTTATTCTTGTCAACAAACTCAGAATAACTAAAGTTAAAGTTGCTTTATAACCTCTATTATTTCCA
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18565 CAAGGGTGCAGCCTCATTGTTGTTGTTTGTGTTGATGAGATGAGTAACAGAGAGTGCGCTCAGCACTTTAAAATGAATACTTGTGGCCAAA
18656 ATATTAAAGCAAATAGCCTGAACCCCCACACCCCAGCCCCAGGCAAACATAAATTATGGTTAAACTTCCATTACAGAGAACTCCACAAACA
18747 TGGATTTGATTAATTTGCTGAGCAGTTCATGACCCTTATGTTATACTTTGCACTATGTAACAAAGAAGCTAAATCTTGAACAGCAAGCTTA
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18929 TGAAAGCCTCTTTGTATCACTGGGATTGCAGCACGCATGATCAAGGCCCAGGGGTGATCACCAGGCCACACTGCTCCTAAGACAGAGGTAC
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19293 TACAACATGCTGAACGCGGACACTACTCGCAACCTCATGATCTGCTTCCTCTGGATCATGAAAAATGCTGATCAGAGCCTCATTAGGAAGT
19384 GGATTGCTGACCTGCCATCAACGCAGCTCAACAGGATTTTAGATCTACTTTTCATCTGTGTGTTATGTTTTGAGTATAAGGTAAGTCTGGA
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19657 AACCCCATTTCTGTTGACAGAGTTTTGGCCCATAGGATGCTCCAGAGCAGCATCTCAGTGAAGCACATGTCAAACTTAGCTGGCATCACTG
19748 TGGAGTGTACTGTTTTGGTAACTCTCCCCATCAACGGAGATCTCACCAAAGGACATGTCCTCCTACCTCTGTCTTGTCCAGGGAAAACAGA
19839 GTTCTGACAAAGTCAGTACCCAAGTCCTGCAGAAGTCAAGGGATGTCAAGGCCCGGCTGGAAGAGGCTTTGCTCCGTGGGGAAGGGGCCAG
19930 AGGGGAGATGATGCGCCGCCGGGCTCCAGGTGTGTTGGACTGGCCCTTCCCTGCTCTCTGTCAAGCAGTTTTTCACTGTTTGTGGGGAGGA
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20112 TTTGTGTTAGCCCTGTGCCTGTGAGGGAAAGCGCTGTTCTACAATTGTAGGAACCCTGAAAACAGCACCAAATGACATCTTTTAATTAAAA
20203 CTCGTTGATGGTAAAAGGTCACCTCTAAGAATGTCAGTCATGGATGAGGTGGAAGGTGTTTCCCTCAAGGCTGAGGCCTTTCTATGTGACC
20294 TTTGGCTAGTCTATCCGGAGCATGGTCAAGAAACTGAACAGTTCTGGCCCCAAGATCATCTTCTCGATCATTCAGGGCACTATTAGAATGG
20385 AACCAGTTCCCTGAAATGGCTTCAGAGTGTCCCAGTCATTCAAGGATTCCACCACAGGAGGAATGATCTCAAAAAGGCTGAGCTTGAATAG
20476 AATGAAATCCCCAGGTACCCTCAGTCTTATTCACCATGCTCAAAGTAAAACAGAGTGACAGCTTATTGTATTCGAAGGGACACAGTGGCAG
20567 GGAACTTGGAGGGAGCTCATAGTTTTCAGTGGTGGTCAGGCACCCTCATTTGACACCCATACTTTCATACCCAATAATTCAGTAAGCCCCC
20658 AGAGTTTCACAGGAATCCTCTGCTCATGAGAAATGTCTCTCTGACACTCAGAAAGGCAGAGGTTCTTCTTATATTCTAGTCTATCAATCAA
20749 AGAGCGGGCCAACTTGGACATAGGTGTGGCGACTTTGTCTCCTACCAGCAACCTGCATGGACTCTAATTAGCCCGAGAAATGGTGCTGAGG
20840 CTTCTCAGTTGAGCTTGTTATGAACTTCTGGTTATCTTGGAGGGTTTCATGCTAATCAAATTCCTATCATGCATTTCTTAACTCCTAGGGA
20931 ACGACCGATTTCCAGGCCTAAATGAAAATTTGAGATGGAAGAAAGAGCAGACACATTGGCGGCAAGCTAATGAGAAGCTAGATAAGTGAGT
21022 CACTCGGCAACTTTCTGCTACTTTTACCTAAAGTCCAAAACTATTTTTCCCAGGCTGCTTGTATTACTGAAACAACTGCATCCTTCCAAGG
21113 GTTAGAAAATGAAACATCATTATCTGTGTAAATACAATTCATCCAGGGACCCAGGATAATCAAAGGTATAGGGAGTTGTGGTTTCCAGCTC
21204 TTAAAAATTTGTCACATTGATAAGCATGTAAAGAAAACTAATATTTCTTTAGCAACCTCAGATGGCTTAATAAAAGCAGCTGATTTTGCAG
21295 GGAGGGTAGCAGGGAAATAGAGAAAGCAGGACACGGTGCCTAGGACCGTATACTTTCAAATCGATATTTCCTTTCTGGAAATATGTACAAG
21386 ATATACATTCAGATATATTTATGTCAGTGCTACTTAAAGTTGTTTTTTAAAATTGAAAACATTCTAAATGCTCCAGAATAGAAAAATATAT
21477 TTAAAAGTTGGATTGCCATCAAAATGTTTTAAAATCATCTTAATGACATGGGGAAATGCTTATGACATAATGTTAAATGAACAAAGGCAGG
21568 GTAGACACTTGGTTTTCTAGTAGTGTGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCCGGTGGAACACCTGAGGTCAGTA
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21841 GGTGACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAAAAAAAGAACCTCAAATCTCTGATGACATATAGTCAATGTATTTTTTAAAGGCT
21932 AGAAGGAAATTTACCAAAATATTAATTGCGGTTTTCTTTGGGTGCTGGGAATATCGGTAATTGATGTTTTCTCTTTTATACTTTGCTATGT
22023 TTCCTACAGTAGATGTGTATTATAATATATATTGTTACCAGAAAAAAAATTATAAAGAAATGAAAGAATAAAAAAACCTGTTTGGATCAAA
22114 ATCTATGCTATAGATGAATAGATATATTGACGTGTATTGCTATATATGCAACAATTTAGACATATGAAAGCTAAAAGTATATATGTTTGAC
22205 TAGATAGCACATGTTTCCGATACCGTTTAGCCACAGGTAGCCTAATGAGTCCCAGGGTTTGCTGAGCAAAATGTCGTAGAGCTAAAATCAC
22296 CCCTCACACACAGTTGACAAGGTAGGATACCCCATGGGTGATGAAGCACCCATCAAAGGGGGTATGGGGCAGACTTGATTAGCAGTGCTGT
22387 TTTGTAAATAAATGTGAGTTAATATCTTTATTGTTACCACAAGAATGAATCATTCTGGTTAACTTATGGGACTTTGGGGAGTCACATTTAT
22478 TTTAAAACATTAAAGAAATAAGTATATTTTTATTATAGATGTGACTTGGAAACCCAGTTGTTGGTATCATGCCTATTTGCTTTGGGTATGT
22569 TATTCTTGCACTAAATTCCCTGGACTGATTTATAAAATACTTGGATCGGAGAGTCCATACATTCTACTTCGGGCAATGAACAACAACTACA
22660 AAATATGCATGCCGTGGGTGCTACAGAATTGCTTAGGTGGTTTAGCTCATCTACTCTACTAGATTAAAAGAAGACCCCTAAGTAGGCCTGT

FIG. 7
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22751 TTTGCCTGGGCTGTGTAAACTGGTGTTTTGGAAAACCTTTCCCTTTTGCTTGCAGGAGCAACACAATATTGGTCCTTACCACGCATGGCCT
22842 ACCGGTTTGCTCTAGGTTAGTTCTCAGCCCTGCGCTACCTGGTGGGCTGCTGGTTGTCAGAGCTAATGATTCACATCTACAAATTCTCAGG
22933 GGCTTTGTGCTTTTTTTTTTTTTTTAAAAGGGAAACCATAGTAAAATTATAACTGTTCAACCTACCTACCTGGAAAATTTATAATTATAAT
23024 AATGGTGTCTTTCACCCTCTTTCTGATCATTTTTCGATTATTTTGGCTCTGTTTCTTTTAGAGCAATGATCTTCAACTTAGGCTGCACATT
23115 AGAATCACCTGGGGAGCTTTAAAACCTGTCAGTGCCCAGCTGCACCCTAGACTACTTCAATTGGAAACTCCAGCAGGACCCAGAAATCAGT
23206 ATTTGGTAAAACTTCCCAGGTGATTCTATTGCCACCAAATCCATTGTTTTAAAGGAATAGATGGTAAGCTTTTCTTTTCTTTTTTTTTTCT
23297 TTTCTTTTTTTGAGACAAGGTCTCACTCTGTCACCCAGGCTGGAATACAGTGGCACAATCACAGCTCACTGCAGCCTTACCCTCCTGGCCT
23388 CAAACAATCCTCCCACCTCAGCCTCCCAAGTAGATGGGACTACAGGTGTGTACCACCACAACTGCTTACTTTTTGTATTTTTTGTAGAGAC
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23570 ATGAGCCACTGCGCCTGGTCAGATGGTAAAGCTTTTAAAAAACCAGATTAGTGTTAGTGATGGTTGCACAATATGAATGTACTTAACACTA
23661 CTGAACTGTATACTTACAAATGGTTAAGATGGTAAATTTTTATGTTAGGTGTACTTTATCACAATACAAAAATTTGGGAAAAAACAGATTA
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24025 CACAATATATAAAATGACATATGTGGCCCCCATTGTTTCTACTAGACAGCATTGCTCTAAATTTAAAACTAAACTAGCAGTCAATTAATTA
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24298 GCTACTCGGGAGGCTGAAGCAGGAGAATGGCGTGAACCCGGGAAGTGGAGCTTGCGGTGAGCCAAGATTGCGCCACTGCACTCTGCACTCC
24389 AGCCTGGGCGACAGAGGGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAGGATGATGAGGTTAAAATGGTAAATTTGATGTTATGTGTAC
24480 TTTATCACGATATAAAAATTTGATGGCTCATGCCTGTGGTCCCAGATACTCAGGAGGCTAAGGCAGAGCATCACTTGAGCCCAGGAGTTCG
24571 AGGCTTCAGTGAGCTATGATAGTGCCACTGCACTCTAGCCTGGGTGATAGAGCAAGACCCTGTCTCTAAGGAAAAAAAAAAAAAAAAACTT
24662 TTAGATTTCATTTATTTTACACATATATTATCACTTGGAAAATGAGAAAAAGTGTCAAGTGGCTTGGGACCAGAGAGCCTATCCTAAACAT
24753 GAAAACAAGTAAAACACACAGAAGTACTTATTTTTTGAGTCCTCAGTGGTATGTAAGCAGCTGCAGTGCCCCCATTATTAGGTTAATGGGA
24844 CGCAAGAACAGGTAAGTGGTAACCCTGGCCCAGGACATATGAGCTGATATAATGATACCCCAACCCCATGGTAACATCTTGGCTACTGAGG
24935 CATCTTGGTAAAGTCAATTCTTCATACCTCCCTTTCCTTGCAACTAGATTTGGATGATGATACAAAATATCCCTTTACAGCTTCACTTAGA
25026 TTTCATAAGAATGGATGGGCTAGCAAAAAAAACCATTCTGATTCCTTAAAGTGAAACCTAATAGAGGAGCGAGCACCAGGCAATTTCCCAT
25117 TCCCTAGTGGGCAATGACCAGTAATGTCCGGCAGGATATTAGATCACCTGCCCTACAGGAATACAGTCTTGTTTCCCAATGGAAAAGGACG
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25299 CCTTTCCTAACCCAGCCGCATCACTGCCAAGTTCACATCACATCCAGTCTCACTCTCTCTCGCATGTTGCAGGGGCTTCCCCTTACTCAGA
25390 TCTAGCAATGGTTTTCATGCGTGAAATACAGCCATGGCCCTGAGGCTTTAGGCAACAATCTGAGAGGGGAGCTTAATTGCTAGTAGCAACT
25481 AATAACTGCTTCTCTACCCATAGTGTTATTTTTATAATTGTCCTCATCATTATTAATAATAGTGGGGATGAGGATGACCAGGAAACCTTAC
25572 CTAGACAGTTGTTTCGACAAGACATGAATCACAGAAGGCACCTGCACTGTAGTTACTCAGGGCCAGTTGCTCTGTTTTCATTTCAAGGTTG
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25754 TTGTTTCCTAGAACAAAGGCCGAGTTAGATCAAGAAGCCTTGATCAGTGGCAATCTGGCTACAGAAGCACATTTAATCATCCTGGATATGC
25845 AGGAAAACATTATCCAGGTGAGGAAAACAAACACCCAATCTGATTTGTTGGCCATGAATATGTTTACTAGAATAAGGACTTCTTTATGCAA
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26391 ACTTTGTACCATACTAATTTTATCTTCTATGTGATTATTTCCACAAATTCCCAAGCTGTCTAGGTAATAATGAGTTTTTAATTACCCTGAA
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26573 AGTGAAATCTTAATTCTCTAACTTTTGAATTGTCTAAAATCAAAGTAATCATCATACAAAAATAAACACAAAAAGTATGTGATATTTTTGT
26664 TGACTTTAATATCTTTGATAACTTAAATGCTTGGTATCACATTTACCTTATCTTTATATAGCACAATATTAGGTGCCAAATATCTATACTA
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26846 CTTCTATTTAGAAACATTGCTGCCACCAAGCAGCCCCTGTTGTACTGGGAAGCCCACAATTGTGTTTTGCATCCCATAAGGAAAGCTATGT
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27210 GATTCAATGATGCTGTTCTTCCATTCCCCCAGGCGAGCTCGGCTCTGGACTGTAAAGACAGCCTGCTGGGAGGTGTTCTGAGGGTGCTGGT

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FIG. 7
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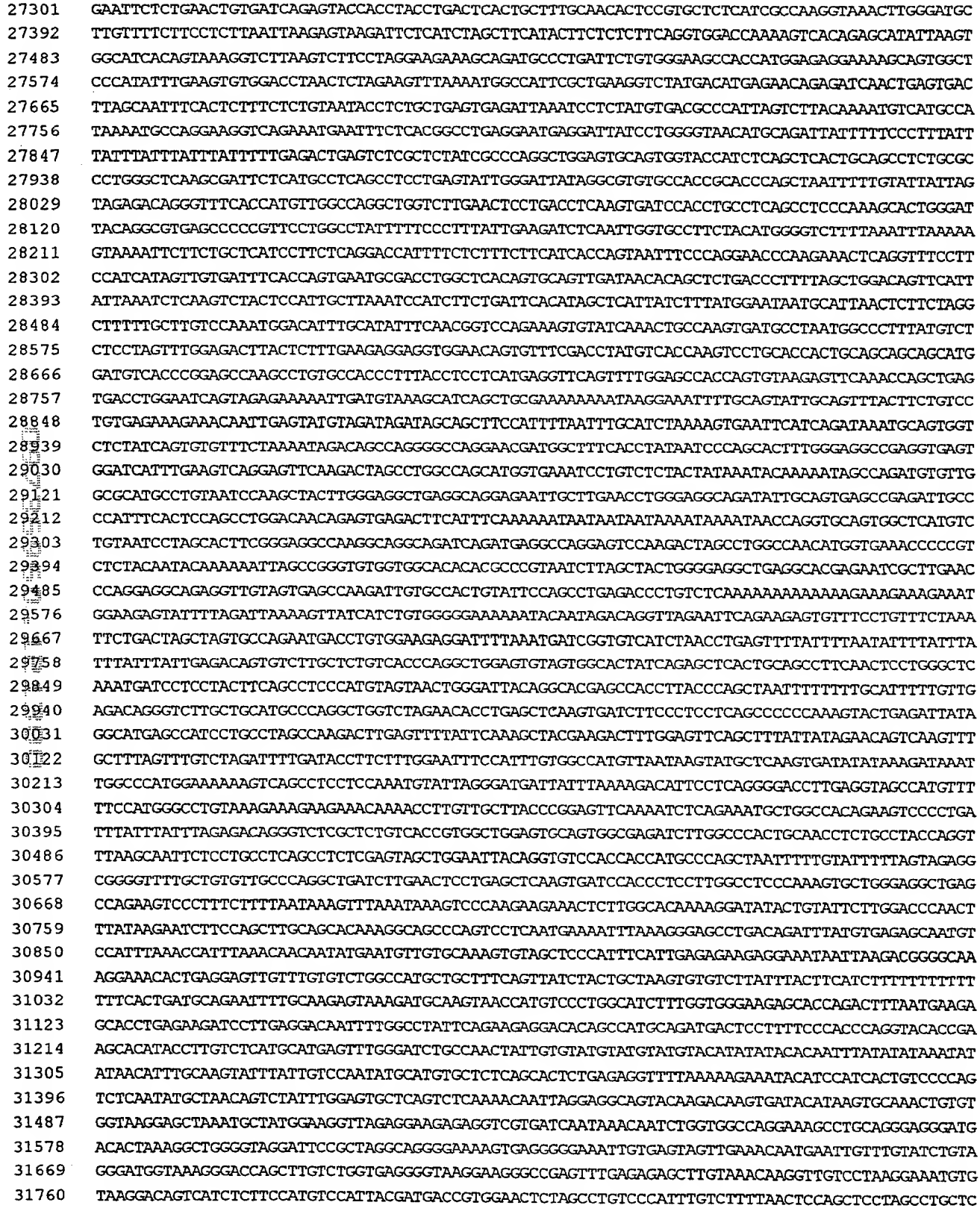
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28120 TACAGGCGTGAGCCCCCGTTCCTGGCCTATTTTTCCCTTTATTGAAGATCTCAATTGGTGCCTTCTACATGGGGTCTTTTAAATTTAAAAA
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28302 CCATCATAGTTGTGATTTCACCAGTGAATGCGACCTGGCTCACAGTGCAGTTGATAACACAGCTCTGACCCTTTTAGCTGGACAGTTCATT
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28575 CTCCTAGTTTGGAGACTTACTCTTTGAAGAGGAGGTGGAACAGTGTTTCGACCTATGTCACCAAGTCCTGCACCACTGCAGCAGCAGCATG
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28757 TGACCTGGAATCAGTAGAGAAAAATTGATGTAAAGCATCAGCTGCGAAAAAAAATAAGGAAATTTTGCAGTATTGCAGTTTACTTCTGTCC
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29212 CCATTTCACTCCAGCCTGGACAACAGAGTGAGACTTCATTTCAAAAAATAATAATAATAAAATAAAATAACCAGGTGCAGTGGCTCATGTC
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30122 GCTTTAGTTTGTCTAGATTTTGATACCTTCTTTGGAATTTCCATTTGTGGCCATGTTAATAAGTATGCTCAAGTGATATATAAAGATAAAT
30213 TGGCCCATGGAAAAAAGTCAGCCTCCTCCAAATGTATTAGGGATGATTATTTAAAAGACATTCCTCAGGGGACCTTGAGGTAGCCATGTTT
30304 TTCCATGGGCCTGTAAAGAAAGAAGAAACAAAACCTTGTTGCTTACCCGGAGTTCAAAATCTCAGAAATGCTGGCCACAGAAGTCCCCTGA
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30668 CCAGAAGTCCCTTTCTTTTAATAAAGTTTAAATAAAGTCCCAAGAAGAAACTCTTGGCACAAAAGGATATACTGTATTCTTGGACCCAACT
30759 TTATAAGAATCTTCCAGCTTGCAGCACAAAGGCAGCCCAGTCCTCAATGAAAATTTAAAGGGAGCCTGACAGATTTATGTGAGAGCAATGT
30850 CCATTTAAACCATTTAAACAACAATATGAATGTTGTGCAAAGTGTAGCTCCCATTTCATTGAGAGAAGAGGAAATAATTAAGACGGGGCAA
30941 AGGAAACACTGAGGAGTTGTTTGTGTCTGGCCATGCTGCTTTCAGTTATCTACTGCTAAGTGTGTCTTATTTACTTCATCTTTTTTTTTTT
31032 TTTCACTGATGCAGAATTTTGCAAGAGTAAAGATGCAAGTAACCATGTCCCTGGCATCTTTGGTGGGAAGAGCACCAGACTTTAATGAAGA
31123 GCACCTGAGAAGATCCTTGAGGACAATTTTGGCCTATTCAGAAGAGGACACAGCCATGCAGATGACTCCTTTTCCCACCCAGGTACACCGA
31214 AGCACATACCTTGTCTCATGCATGAGTTTGGGATCTGCCAACTATTGTGTATGTATGTATGTACATATATACACAATTTATATATAAATAT
31305 ATAACATTTGCAAGTATTTATTGTCCAATATGCATGTGCTCTCAGCACTCTGAGAGGTTTTAAAAAGAAATACATCCATCACTGTCCCCAG
31396 TCTCAATATGCTAACAGTCTATTTGGAGTGCTCAGTCTCAAAACAATTAGGAGGCAGTACAAGACAAGTGATACATAAGTGCAAACTGTGT
31487 GGTAAGGAGCTAAATGCTATGGAAGGTTAGAGGAAGAGAGGTCGTGATCAATAAACAATCTGGTGGCCAGGAAAGCCTGCAGGGAGGGATG
31578 ACACTAAAGGCTGGGGTAGGATTCCGCTAGGCAGGGGAAAAGTGAGGGGGAAATTGTGAGTAGTTGAAACAATGAATTGTTTGTATCTGTA
31669 GGGATGGTAAAGGGACCAGCTTGTCTGGTGAGGGGTAAGGAAGGGCCGAGTTTGAGAGAGCTTGTAAACAAGGTTGTCCTAAGGAAATGTG
31760 TAAGGACAGTCATCTCTTCCATGTCCATTACGATGACCGTGGAACTCTAGCCTGTCCCATTTGTCTTTTAACTCCAGCTCCTAGCCTGCTC

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FIG. 7
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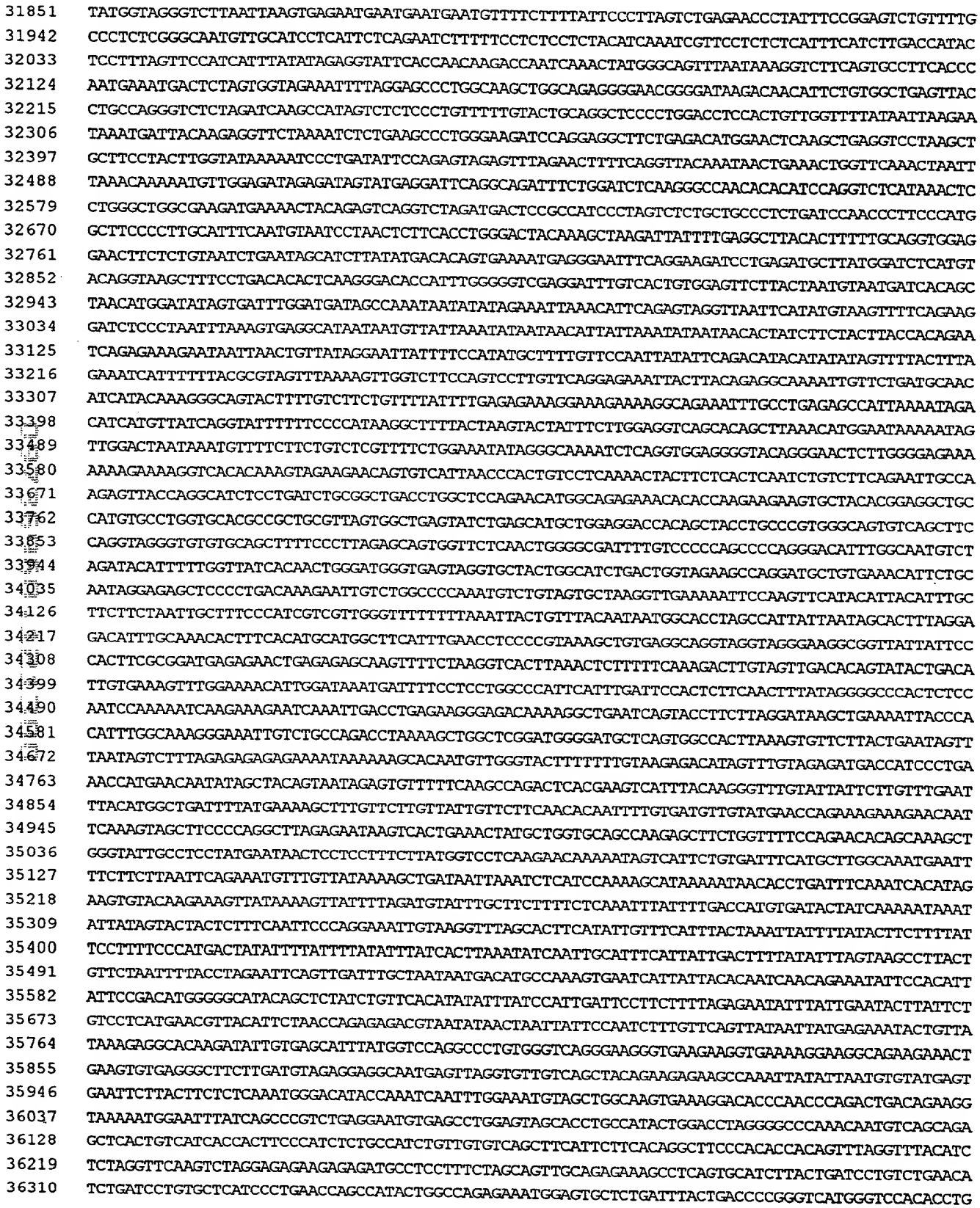
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31942 CCCTCTCGGGCAATGTTGCATCCTCATTCTCAGAATCTTTTTCCTCTCCTCTACATCAAATCGTTCCTCTCTCATTTCATCTTGACCATAC
32033 TCCTTTAGTTCCATCATTTATATAGAGGTATTCACCAACAAGACCAATCAAACTATGGGCAGTTTAATAAAGGTCTTCAGTGCCTTCACCC
32124 AATGAAATGACTCTAGTGGTAGAAATTTTAGGAGCCCTGGCAAGCTGGCAGAGGGGAACGGGGATAAGACAACATTCTGTGGCTGAGTTAC
32215 CTGCCAGGGTCTCTAGATCAAGCCATAGTCTCTCCCTGTTTTTGTACTGCAGGCTCCCCTGGACCTCCACTGTTGGTTTTATAATTAAGAA
32306 TAAATGATTACAAGAGGTTCTAAAATCTCTGAAGCCCTGGGAAGATCCAGGAGGCTTCTGAGACATGGAACTCAAGCTGAGGTCCTAAGCT
32397 GCTTCCTACTTGGTATAAAAATCCCTGATATTCCAGAGTAGAGTTTAGAACTTTTCAGGTTACAAATAACTGAAACTGGTTCAAACTAATT
32488 TAAACAAAAATGTTGGAGATAGAGATAGTATGAGGATTCAGGCAGATTTCTGGATCTCAAGGGCCAACACACATCCAGGTCTCATAAACTC
32579 CTGGGCTGGCGAAGATGAAAACTACAGAGTCAGGTCTAGATGACTCCGCCATCCCTAGTCTCTGCTGCCCTCTGATCCAACCCTTCCCATG
32670 GCTTCCCCTTGCATTTCAATGTAATCCTAACTCTTCACCTGGGACTACAAAGCTAAGATTATTTTGAGGCTTACACTTTTTGCAGGTGGAG
32761 GAACTTCTCTGTAATCTGAATAGCATCTTATATGACACAGTGAAAATGAGGGAATTTCAGGAAGATCCTGAGATGCTTATGGATCTCATGT
32852 ACAGGTAAGCTTTCCTGACACACTCAAGGGACACCATTTGGGGGTCGAGGATTTGTCACTGTGGAGTTCTTACTAATGTAATGATCACAGC
32943 TAACATGGATATAGTGATTTGGATGATAGCCAAATAATATATAGAAATTAAACATTCAGAGTAGGTTAATTCATATGTAAGTTTTCAGAAG
33034 GATCTCCCTAATTTAAAGTGAGGCATAATAATGTTATTAAATATAATAACATTATTAAATATAATAACACTATCTTCTACTTACCACAGAA
33125 TCAGAGAAAGAATAATTAACTGTTATAGGAATTATTTTCCATATGCTTTTGTTCCAATTATATTCAGACATACATATATAGTTTTACTTTA
33216 GAAATCATTTTTTACGCGTAGTTTAAAAGTTGGTCTTCCAGTCCTTGTTCAGGAGAAATTACTTACAGAGGCAAAATTGTTCTGATGCAAC
33307 ATCATACAAAGGGCAGTACTTTTGTCTTCTGTTTTATTTTGAGAGAAAGGAAAGAAAAGGCAGAAATTTGCCTGAGAGCCATTAAAATAGA
33398 CATCATGTTATCAGGTATTTTTTCCCCATAAGGCTTTTACTAAGTACTATTTCTTGGAGGTCAGCACAGCTTAAACATGGAATAAAAATAG
33489 TTGGACTAATAAATGTTTTCTTCTGTCTCGTTTTCTGGAAATATAGGGCAAAATCTCAGGTGGAGGGGTACAGGGAACTCTTGGGGAGAAA
33580 AAAAGAAAAGGTCACACAAAGTAGAAGAACAGTGTCATTAACCCACTGTCCTCAAAACTACTTCTCACTCAATCTGTCTTCAGAATTGCCA
33671 AGAGTTACCAGGCATCTCCTGATCTGCGGCTGACCTGGCTCCAGAACATGGCAGAGAAACACACCAAGAAGAAGTGCTACACGGAGGCTGC
33762 CATGTGCCTGGTGCACGCCGCTGCGTTAGTGGCTGAGTATCTGAGCATGCTGGAGGACCACAGCTACCTGCCCGTGGGCAGTGTCAGCTTC
33853 CAGGTAGGGTGTGTGCAGCTTTTCCCTTAGAGCAGTGGTTCTCAACTGGGGCGATTTTGTCCCCCAGCCCCAGGGACATTTGGCAATGTCT
33944 AGATACATTTTTGGTTATCACAACTGGGATGGGTGAGTAGGTGCTACTGGCATCTGACTGGTAGAAGCCAGGATGCTGTGAAACATTCTGC
34035 AATAGGAGAGCTCCCCTGACAAAGAATTGTCTGGCCCCAAATGTCTGTAGTGCTAAGGTTGAAAAATTCCAAGTTCATACATTACATTTGC
34126 TTCTTCTAATTGCTTTCCCATCGTCGTTGGGTTTTTTTTAAATTACTGTTTACAATAATGGCACCTAGCCATTATTAATAGCACTTTAGGA
34217 GACATTTGCAAACACTTTCACATGCATGGCTTCATTTGAACCTCCCCGTAAAGCTGTGAGGCAGGTAGGTAGGGAAGGCGGTTATTATTCC
34308 CACTTCGCGGATGAGAGAACTGAGAGAGCAAGTTTTCTAAGGTCACTTAAACTCTTTTTCAAAGACTTGTAGTTGACACAGTATACTGACA
34399 TTGTGAAAGTTTGGAAAACATTGGATAAATGATTTTCCTCCTGGCCCATTCATTTGATTCCACTCTTCAACTTTATAGGGGCCCACTCTCC
34490 AATCCAAAAATCAAGAAAGAATCAAATTGACCTGAGAAGGGAGACAAAAGGCTGAATCAGTACCTTCTTAGGATAAGCTGAAAATTACCCA
34581 CATTTGGCAAAGGGAAATTGTCTGCCAGACCTAAAAGCTGGCTCGGATGGGGATGCTCAGTGGCCACTTAAAGTGTTCTTACTGAATAGTT
34672 TAATAGTCTTTAGAGAGAGAGAAAATAAAAAAGCACAATGTTGGGTACTTTTTTTGTAAGAGACATAGTTTGTAGAGATGACCATCCCTGA
34763 AACCATGAACAATATAGCTACAGTAATAGAGTGTTTTTCAAGCCAGACTCACGAAGTCATTTACAAGGGTTTGTATTATTCTTGTTTGAAT
34854 TTACATGGCTGATTTTATGAAAAGCTTTGTTCTTGTTATTGTTCTTCAACACAATTTTGTGATGTTGTATGAACCAGAAAGAAAGAACAAT
34945 TCAAAGTAGCTTCCCCAGGCTTAGAGAATAAGTCACTGAAACTATGCTGGTGCAGCCAAGAGCTTCTGGTTTTCCAGAACACAGCAAAGCT
35036 GGGTATTGCCTCCTATGAATAACTCCTCCTTTCTTATGGTCCTCAAGAACAAAAATAGTCATTCTGTGATTTCATGCTTGGCAAATGAATT
35127 TTCTTCTTAATTCAGAAATGTTTGTTATAAAAGCTGATAATTAAATCTCATCCAAAAGCATAAAAATAACACCTGATTTCAAATCACATAG
35218 AAGTGTACAAGAAAGTTATAAAAGTTATTTTAGATGTATTTGCTTCTTTTCTCAAATTTATTTTGACCATGTGATACTATCAAAAATAAAT
35309 ATTATAGTACTACTCTTTCAATTCCCAGGAAATTGTAAGGTTTAGCACTTCATATTGTTTCATTTACTAAATTATTTTATACTTCTTTTAT
35400 TCCTTTTCCCATGACTATATTTTATTTTATATTTATCACTTAAATATCAATTGCATTTCATTATTGACTTTTATATTTAGTAAGCCTTACT
35491 GTTCTAATTTTACCTAGAATTCAGTTGATTTGCTAATAATGACATGCCAAAGTGAATCATTATTACACAATCAACAGAAATATTCCACATT
35582 ATTCCGACATGGGGGCATACAGCTCTATCTGTTCACATATATTTATCCATTGATTCCTTCTTTTAGAGAATATTTATTGAATACTTATTCT
35673 GTCCTCATGAACGTTACATTCTAACCAGAGAGACGTAATATAACTAATTATTCCAATCTTTGTTCAGTTATAATTATGAGAAATACTGTTA
35764 TAAAGAGGCACAAGATATTGTGAGCATTTATGGTCCAGGCCCTGTGGGTCAGGGAAGGGTGAAGAAGGTGAAAAGGAAGGCAGAAGAAACT
35855 GAAGTGTGAGGGCTTCTTGATGTAGAGGAGGCAATGAGTTAGGTGTTGTCAGCTACAGAAGAGAAGCCAAATTATATTAATGTGTATGAGT
35946 GAATTCTTACTTCTCTCAAATGGGACATACCAAATCAATTTGGAAATGTAGCTGGCAAGTGAAAGGACACCCAACCCAGACTGACAGAAGG
36037 TAAAAATGGAATTTATCAGCCCGTCTGAGGAATGTGAGCCTGGAGTAGCACCTGCCATACTGGACCTAGGGGCCCAAACAATGTCAGCAGA
36128 GCTCACTGTCATCACCACTTCCCATCTCTGCCATCTGTTGTGTCAGCTTCATTCTTCACAGGCTTCCCACACCACAGTTTAGGTTTACATC
36219 TCTAGGTTCAAGTCTAGGAGAGAAGAGAGATGCCTCCTTTCTAGCAGTTGCAGAGAAAGCCTCAGTGCATCTTACTGATCCTGTCTGAACA
36310 TCTGATCCTGTGCTCATCCCTGAACCAGCCATACTGGCCAGAGAAATGGAGTGCTCTGATTTACTGACCCCGGGTCATGGGTCCACACCTG

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FIG. 7
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36401  GAATTATGGGTGATTTCTTCCCCTAAATCAGGATGCCTTACTTTATAGAAGGAGGAAAGAATTCTAGACAGCATTAACAACAGATGTCCAG
36492  TGTTGATTTTGCAAATGCTCTGTGCTTTAATTTTCAACCTTGTTCTGCTCCAATGAAATAGAGCTTTTGGAAAAGATTTATAAACTAGAGA
36583  TAAATAAATATGTGCAAGGAAAATAACTTTGAGGTCACTGAATTCCAGGAAACTGAGATCACTGAAATTCTGTGTCCCAGAGTGCAATATT
36674  TATTTCACAACTGTAGATACGGACACATTCTTAGATACTGCTGTTACTTGTACCTCCCTGATCCTGAAGCCAAGAAAGTCTGCAGAATCCT
36765  TTTCCTCTGACTACAGCTAATGAGGCTACATAGCTTCAAATCTGTTCCTCTAATGTGGAAAATTGCATACATTCTAATAGTATTAGTATCT
36856  TGGGTTATTAAATGCTTTCAACTGAATTTCTTGGATCTTCTGTTGTCACAGAAACATCATAATACATAGGGCAGGTTTGGAAGAAAGACTG
36947  GCCACAAAGGCTTTGAGAGCCTCCTCCTATATTCCTAAAACTACGTTACAGTATTGCATGTGAAGAGATAGGGCTATCTATGACAACTATG
37038  TCCTGACTGATTGCTAAGGTTGATTCACATGATCTTGCTAACCAGGCCAGAAGGCAGACAGCTTTTAGTTCACAAGCCAACTCTGATCAGT
37129  TAGTAGTGGCTGACTGGAGAACTATGCTTAAGAATTTCGAGACTATGTCCAAGCTCTGGGGAAAAAGTGCTACAGTTGATTAGTTATGCCT
37220  GCCATGATTACAGCAATAGGAAGGAGTGGCATGTGTGCCACCTGTTTGTAATCCCTAAACTGGGAAGGTTTCCCATTTCTTCTGTTTTTCA
37311  TATGCATTTCTTCCATAGCTGTGAGCTAGGAAGAAAATGATTCTTGACCTGTCACATATTCACTGCCAGGGCCAGTGCTAGGGTGAAGAGG
37402  CACTCACCCTCAGGGTCGAGCGGGTACAAGATCAGTACTTCCATGGCCCTAAAAGCGAGTACCTCTCTAAATTTTGTCTTGGGTTTCTCAT
37493  TTGGTTCACCCCAACCATGGTCTCTGCATGCTCTGCTAGAGGCTCTAAACGCAATAGTTTATGTAAAGGAAACAAATGCATGGAAACAAAA
37584  TGTTCAGGAAGAACAAAAACACACACACAGTAACTGCTGCAATGCCATGAAAACTTCCTTAATGAAGACAGCCTCGCTTGCTGTTGTCGTA
37675  TGTCATGGCTGTTTATCTGAGTCAACTCCAGAGTAGCAACATACTTCAGAAAAACACCACTGTAAGTCAGAGGTCCACTCGGTGAAACAGG
37766  GAGCCTAGTTAATGTTAATTGGGTCTTTGCCTTTTGAAAACCAGGACACCAGCCCTATGTCCCTTAGGGTTGTTTCACTAAAGTAACTCAG
37857  CTGTTGTGACATTGAGGTAAGTGTCCTTTATACAAAATCTCCTAATGGTTAAAAAGAAAAACGTGAGGTTTGAAGACCAGTTGCTCAGTGC
37948  GCCTCTTCTAAATGAATGGCAGACAGATACTCTCGGGGTAGAATTACAGACCTAGTTTAGTCACGGTCTTGGTAAGGATCTGCACACCAGC
38039  TTCCTCGTTTCCCCATTCGGGGTTCCTGTGGTCTCTTACTAGTCTGGTCGCCCTGTTCTCCAGGCTTATACTGTGGTCTCTTTCAGAATAT
38130  TTCTTCCAATGTGCTGGAGGAGTCTGTGGTCTCTGAGGACACCCTGTCACCTGACGAGGATGGGGTGTGCGCAGGCCAGTACTTCACCGAG
38221  AGTGGCCTGGTAGGCCTCCTGGAGCAGGCCGCGGAGCTCTTCAGCACGGTCAGTGCCCAGAGGGCATCCCGGGGCCTGGCCTCCCATACTC
38312  CAGCTGGACTTGGGGTGCTGGGAACACCTGGTCTTAATGGCCCAGTCAGCCCCACTTCCCGAGGACACGTGCCAGGGTGTGCGGGGCAGGG
38403  GATGGGCCCGGGGAGGACTTTGATGTATGCAAATTGCATGAGCTTCCCAAGGGAGCTGAGATAACCTTTCATCACAGTGCCGATCTGAGCT
38494  TCACTGTATGCTCATTGGTTGGGCAGCAGTTTCACAGTATTATTTCTATTTAATAGGGGTGGAACTAAGCCACAGAGAGGTGAAATGGCCT
38585  GCCCAGGGTTACACAATAAATGATGAGGCATGTTTTCACTCCCTCGTTTTTCCTCTCAGAGAGAAAAAAATTAGGGAGGAACCACTGGGAG
38676  GAGAGAGGAGGAATACACAGACAGTGTCTTCCCTCCTAGCCACTGTGCAGTCTGAAGGACCATCACAGACCAGGACCAGCTTACAGAAATG
38767  TGGGCACAGAAACCACTGAGACTCCTCTGGTTAACGTAATCTGGATCTAAACACTCCTAGTATATATACTAGAAAAATATATAGAGAGATG
38858  AAGTCATTGAGATTCAGGGCAAAGAGGAAACACTCTTGTCTATTTTCTTTTCTTTTTTTGAGACAGAGTCTAGCTCTGTCGCCCAGGCTGG
38949  AATGCAGTGGTGCAATCATGGCTCACTGCAGCCTCTACCTCCAGGGTTCAAGCAACTCTCCTGCCTCAGCCTCATGAGTAGCTGGGATTAC
39040  AGGTGTGCACCACCACACTCGGCCAATTTTTTGTATTTTTAGAGGAGACAGGATTTCACCCTGTTGGCCAGGCTGGTCTCAAACTCCTGGC
39131  CTCAAGTGATCTGCCCATCTTGGCCTCCCAAAGTGCTGGAACTACAGGTGTGAGCCACCACGCCCAACTTGTTTTCATTTTAATAATCTCC
39222  CTCCTCCTTTACATTTTAAGCCAAGAAAGTATTCAGTACTTTACTATATTTAGCTGACCCAATTTTGTTTTCATCTATACTATACTCATCC
39313  TTATTTTCCAGTTTTTATTTCCAAGTTTCCTCTCTACAATTTTATTTATTTTAATTATTGTTTTAACTGTCTTCTCTCTATTCTTGCTTTC
39404  CTTTTCAAGATTCAGAAAATGTCTAATATACTCTCATTTTTCCTCAAACTCAACAAAATGAATTAGAATCCTACTAACTCTTTGGAGGCAT
39495  ACATTTAGCATCTGGCTAGAGGAGGACCTCTGATGAAATTTAAATATACTAAAACTGCCTTTCTGAATTGCTGTTAGTCCCTGCTACCAAA
39586  CTTCTCTCCTGTTTTTTCTTTTCGTTTTGTTTTGTTTTTGTTTTTGTTTTTGAGGCAGCGTCTTGCCTTGTCACCCAGGCTGGAGTGCAGT
39677  GATGCAGCCTTGGCTCACTACAGCCTTGACCTCCTGGGCTCAGCCTCCCACCTCAACCGCCCAAGTAGCTGAGGCTACAGGAGCATGCTAC
39768  CACACCTGGCTGATTTTTTAATTTTTTTGCAGAGATGGGGTCTCCCTATGGTGTCTAGGATGATCTGAACTTCTGGGTTCAAGTGATCCTC
39859  CTGCCTCAGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCACTCAGCCAGTATTTTTTTTTCCCCCGAAAGCTCTTCTCCTTAC
39950  TTATCGCCATACAGGACTACTTAGCGAGGTGTCTAGTTCAGTTTGAAGGCTACCACTGTCCCAAAAGTGCTCAGATACCCCTTCTTGCCCT
40041  GTGAAATACTGTGATACAACAATAAATTCACTCTCCAGCACATTGTTTGGACAATGACCTCTGGTTGCTCTTCTTAAGTTTCCAGTGGATT
40132  AAATTCTCTCTGATGCTCTTCTCCTCTTTCCAAGGGAGGCTTATATGAGACAGTTAATGAGGTCTACAAGCTGGTCATCCCCATCCTAGAA
40223  GCGCATCGAGAATTCCGGAAGCTGACACTCACTCACAGCAAGCTGCAGAGAGCCTTCGACAGCATCGTTAACAAGGTAGCCGGGGAGCCTG
40314  GCTGGCAGGTCTTGTTACCTGGTGGCAGGCGACCCTGTCCTACAGATGCTTAGCCATCCTTCCTCTCCAGGGAGTGATTTATCTTTAGCAC
40405  ATTGCTTTTGCTCTCACCTGTCAAACAGAAAAGGGCTGAAATTCTTCTAACAGAGGACCAAAATTCCATATGTGAAAACATACAGCTTAAA
40496  TTACTTTATAACCAGGAAATGTGAGAAATTTTTAAGTGTAATTAAAAGAAGTCCCAGAAATCTTTCATGGGATTCCTTTTGTTGTTATTTC
40587  TGAAGTTTATTCCATAAGCATTAAATTTTTTTAAGGAGTAATTTCTGTTTACATCAGCCATAGGAGTAAAATGCTTTGTTAACACAATGAG
40678  AGACCCCTGCCCTTTGCAACTCAGTGGCTCCTCAGGATGACATAACTAAGGAGAGCTTTTTATATTTTGTTCCTCAGGATCATAAGAGAAT
40769  GTTTGGAACCTACTTCCGAGTTGGTTTCTTTGGATCCAAATTTGGGGATTTGGATGAACAGGAGTTTGTCTACAAAGAGCCTGCAATTACC
40860  AAGCTTCCTGAGATCTCACATAGACTAGAGGTAAGAAAAGTGATTCTGTGCGCCTGACCTGGTACACTTTACAAAAACAAGTTAGAGTGGG
```

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FIG. 7
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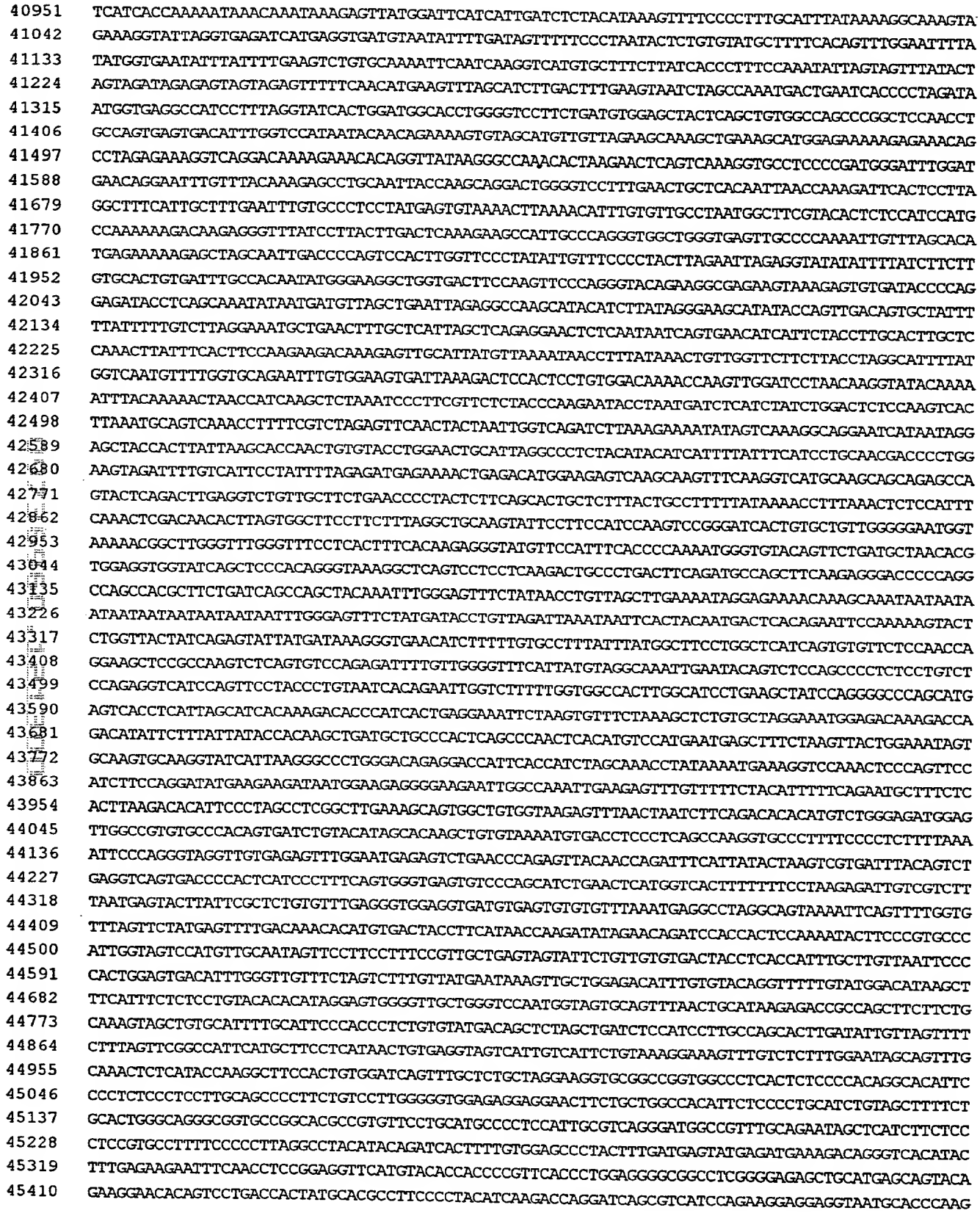

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FIG. 7
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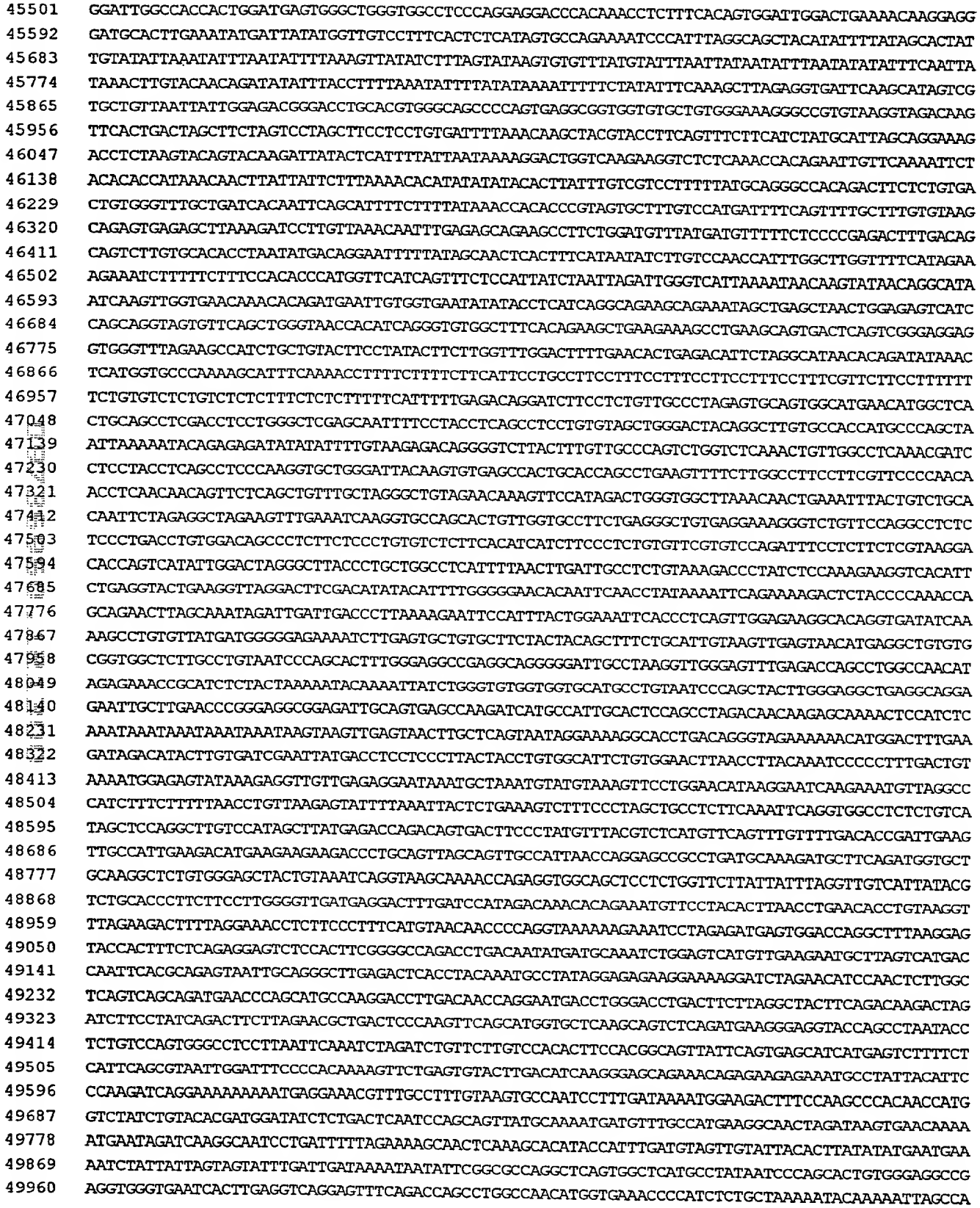

FIG. 7
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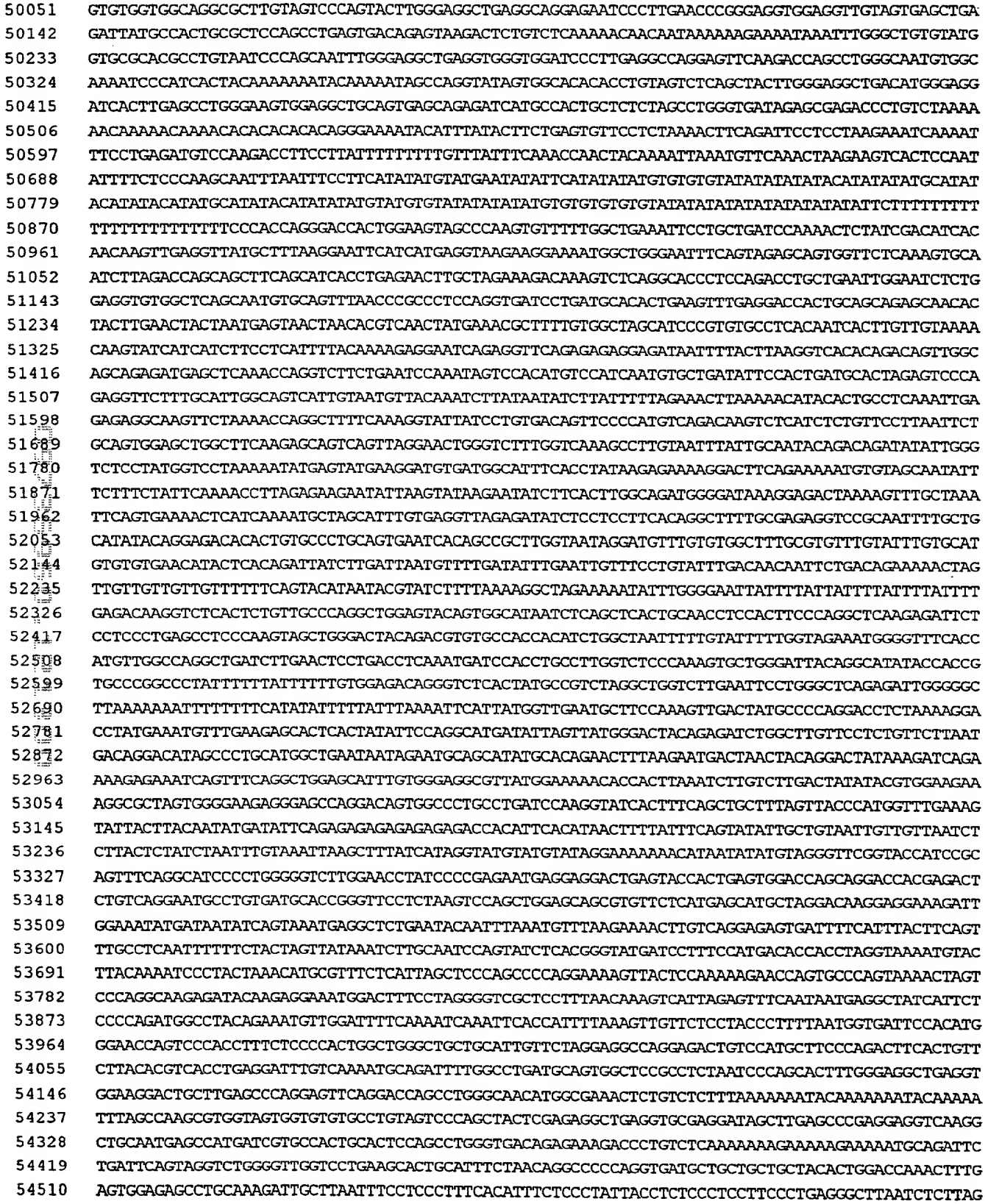

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FIG. 7
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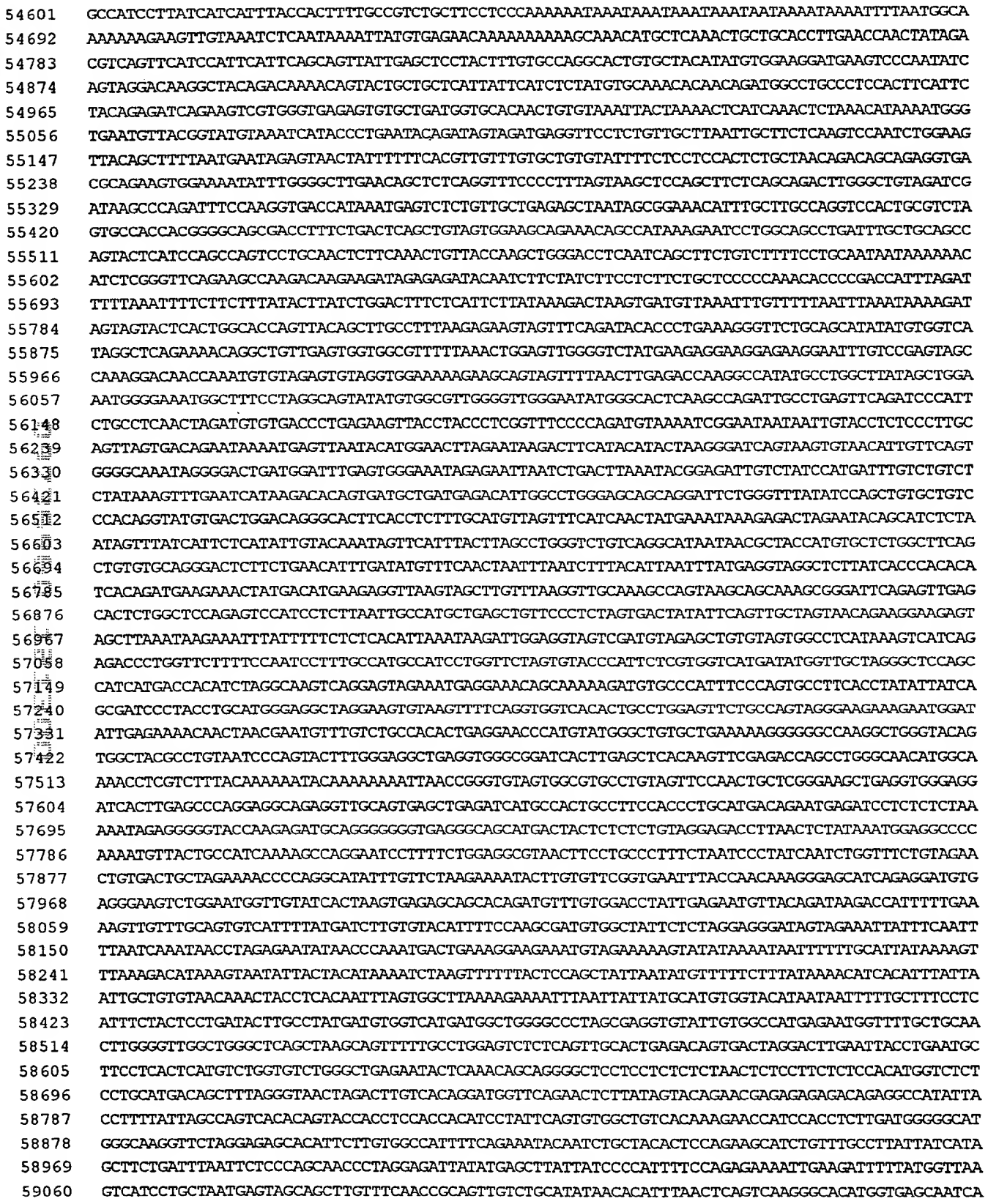

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FIG. 7
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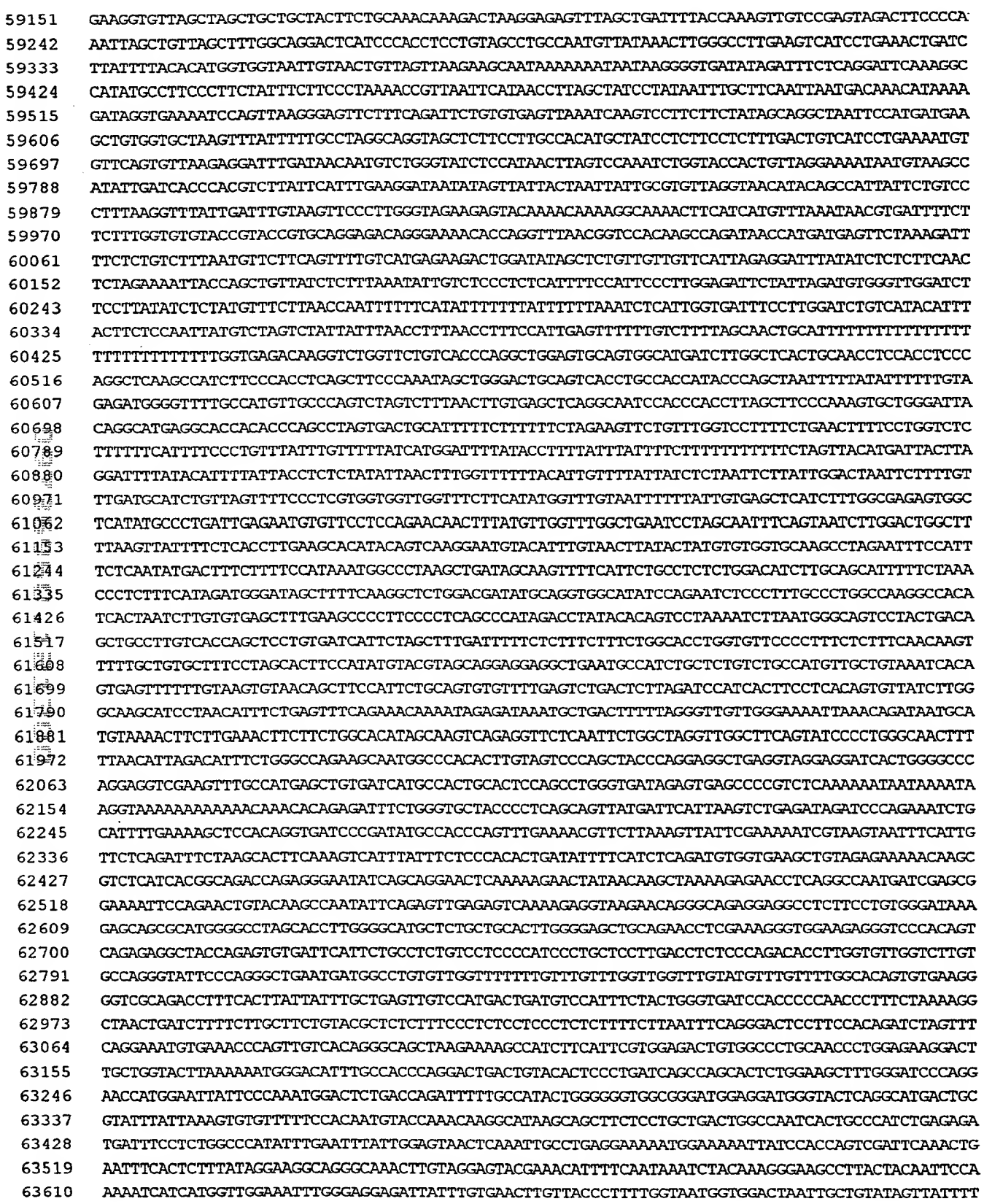

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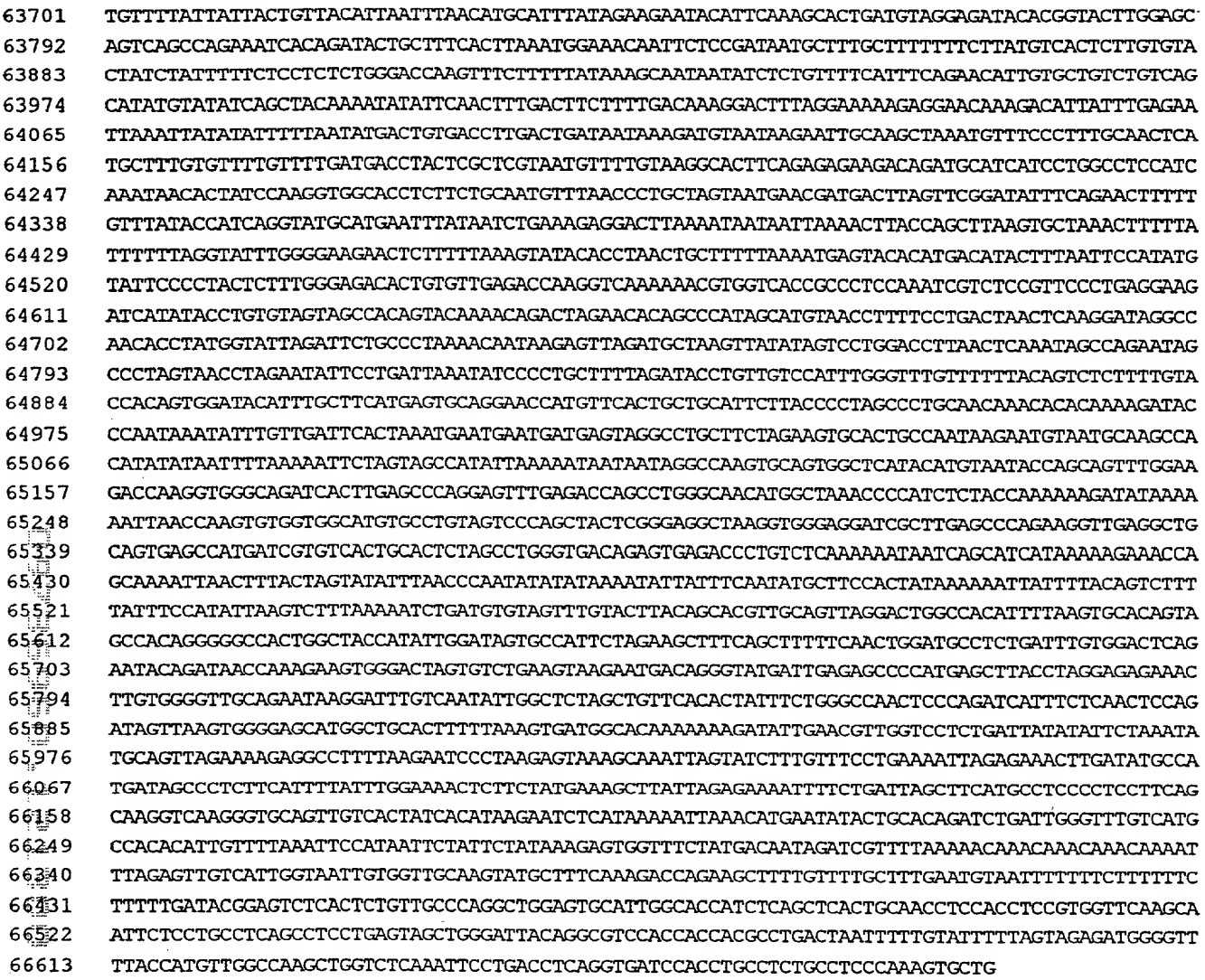

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FIG. 7
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Putative promoter sequence of human CLASP-5

GGAACAATTTCCTCTCATGTGTATGGCTCCCTAAAGTGTTGGCTGAGCATTGTCCACATGGGTG
ATGCAAAGGATCACTGAACTAGGAGCAGTTGGGAAAAAATACAATCATTGGGAATTCCTGTAGC
ATCGAATGTGCCTACAGGGAGGTAGAAGTATTCATACAACAGTTCTCTGGTGTTCTCTGTTGTA
GCAACCAGTCAGCCAAAAGGGTTCAGCTGCTTGAAATGAGAATGGCTGGATCAAAATGGCAGCT
CATGATTTAAAGGATTCTAGTCAGATACCAGACATCCTCACATAGAGAAAACTCTGAATGGCTG
GGGGAGAAGGAGTCAAATGCCCTGGATCTTTTTCTTGGGCCTCAAAGTCCTCCTTCTGTCATCA
TCCTTCCAGTATTGGGCAGGACCTGACTGCAGGCATCATGGCCTCTGTGAACTTCTCAAGGGTA
TGTATTATCTGACAAAAACTACGATGTCCACTAACAGGCCACTGAAAGGTATCTTAGTCAGTTC
TGCTCATTGCCCAGCCAAGGCCTACGTTTTATAACATGATATCAAAGATTGCATCTAAAATTGT
GATGATTTCCTAAAATAATCATTTCATTTAGATTTTTCTATTTTAATCCAAGGTATTCTTCAGC
GGAAATAAGGAAACAGTTTACTCTCCCACCAAACCTTGGCCAGTACCATCGACAGAGCATAAGT
ACCTCTGGCTTCCCCTCTCTTCAACTAGTAAGTATGAGTTCCAGGTTTACTTAGCGATTGGTCA
AGTGCAAAAGTGCCCAGGGTATGTGTTTGCCTCCTGTTCCTTAGATCTTCCTACCATCACCTCA
CATTCTCCAGTCACCAGATCCTAACTCTGTGACTGTGTCTGGACATCAGACAATATCCCTCTCT
CTCTCTGCCAACCGGTACTTAGGGTACATAATAGAACCTCTGGGAGCTGTGGTTTTGATGTCTC
TAGACTAGGTGGGCTTCCAGGTGACTCAGTCTCATCCAAATTATGGTTCATATTTGGGGGAGAA
GGGCTAGCCCAAAAACTTACCACCATTTGTAGTATGCATTTTTTTGGAAAAGCATATTCCAAAA
TCTGAAATGCCAAGTTACAGACCTCCTTTTTGTAAAATAATTTTCTTGCTAGTATAATTTACAT
ATAATAAAATTCACACATTTTAGGTGTACAATTTGGTGAACTTGGGCAACTTAGAGTCACTTAA
CCTTTCCTCAGTCAAGATATAGAACACTTCTTTTATCCTAAAGCGTTCCCCAGCGCGCTTTTAC
AATCTCCTCTCCCCAGGCCACACCCTCCAACTCACGCAATCTCTGACTCACTTCTGTCACCATA
ATTTTGCTCTATCTGGAGCTTCATATCCTGTTACAGTATGTACAAACCTTCTTTTTTTGAGACA
GGGTGTCAGTCTGTCACCCAGCCTGGAGTACAGAGGTGTGATCTCAGCTCACTGCAACCTCAAC
CTCCCAGGATCAGATGATTCTCCTCCCACCTCATCCTCCCAAGTAGCCGGGACTACAGGCGCAT
GCCACCACACCTGGCTAATTTTTGTACTTTTTGTAGAGACAGGGGTCTCGCTATGTTGCCCAGG
CTGGTCTTGAACTCCTGGGCTCAAGCGATCCTCCTGCCTCAGCCTCCCAAAGTGCTGGGATTAC
AGTGAGCCACTGCACCTGGCCCTAAACCTTCATTTTTAAAACACATTTCCTCTTAAATTGAAGA
TTGCCTACATTTTTATATCAATGCCAATTGTTGAGTGTGCCTATATGTGTTATATTATTTGAGC
ACTAAATGCCAGATGTGTGCCAAGTGAGATAAATCTGACAAATGAGATGGTTTGTAAAACCAGC
AGTGAATATTCACTTCCTCTGTGAGAGAGCTCCAGCCCTCCTGTACTCACTTCCTCACACAGCA
CAGCAGCACTCTTGCTGGTTCTGCTGCTTATCTTGAAGAGGTTAGGTTACTTTTTGTTTCTACT
TATTACTTCGAAACCACTTCTGCCTTAGAAATTTTGTAACCTTCCGCTCAGTTTCCGGTAACCG
CCATTTTGTCTCCTGTAACAATTTACGCGCCGTGTAACTGTGAATCTTT

C

FIG. 7

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hCLASP4          ----------------------MFPMEDISISVIGRQRRTVQ----------------- 20
hCLASP5          ----------------------MTHLNSLDVQLAQELG--------------------- 16
hCLASP3          --------------------MAERRAFAQKISRTVAAEVRKQISGQYSGSPQLLKNLNIVG 41
hCLASP2          ---------------------MLLFPYDDFQTAILRRQGRYICS---------------- 23
hCLASP7          -----------------MAASERRAFAHKINRTVAAEVRKQVSRERSGSPHSSRRCSSSL 43
hCLASP1          MSFRGKVFKREPSEFWKKRRTVRRVIQEEFHRFSSQEKPRLLEPLDYETVIEELEKTYRN 60
                                        ..:      .

hCLASP4          --------------------------STVPEDAEKRAQSLFVKECIKTYSTDWHVVNYK 53
hCLASP5          ------------------------------------------------------DFT 19
hCLASP3          N-------------------ISHHTTVPLTEAVDPVDLEDYLITHPLAVDSGPLRDLIEFP 83
hCLASP2          --------------------------TVPAKAEEEAQSLFVTECIKTYNSDWHLVNYK 55
hCLASP7          G-----------------------VPLTEVVEPLDFEDVLLSRPPDAEPGPLRDLVEFP 79
hCLASP1          DPLQDLLFFPSDDFSAATVSWDIRTLYSTVPEDAEHKAENLLVKEACKFYSSQWHVVNYK 120
                                                                      ::

hCLASP4          YEDFSGDFRMLPCKSLRPEKIPNHVFEIDEDCEKDED--------SSSLCSQKGGVIKQG 105
hCLASP5          DDDLDVVFTPKECRTLQP-SLPEEGVELDPHVR---------------DCVQTYIREWLI 63
hCLASP3          PDDIEVVYSPRDCRTLVS-AVPEE-SEMDPHVR---------------DCIRSYTEDWAI 126
hCLASP2          YEDYSGEFRQLPNKVVKLDKLPVHVYEVDEEVDKDED--------AASLGSQKGGITKHG 107
hCLASP7          ADDLELLLQPRECRTTEP-GIPKD-EKLDAQVR---------------AAVEMYIEDWVI 122
hCLASP1          YEQYSGDIRQLPRAEYKPEKLPSHSFEIDHEDADKDEDTTSHSSSKGGGGAGGTGVFKSG 180
                  :: .                :* .  ::* .

hCLASP4          WLHKANVNSTIT--VTMKVFKRRYFYLTQLPDGSYILNSYKDEKNSKESK-GCIYLDACI 162
hCLASP5          VNRKNQGSPEIC--GFKKTGSRKDFHKT-LPKQTFESETLECSEPAAQA--GPRHLNVLC 118
hCLASP3          VIRKYHKLGTGF--NPNTLDKQKERQKG-LPKQVFESDEAPDGNSYQDDQDDLKRRSMSI 183
hCLASP2          WLYKGNMNSAIS--VTMRSFKRRFFHLIQLGDGSYNLNFYKDEKISKEPK-GSIFLDSCM 164
hCLASP7          VHRRYQYLSAAY--SPVTTDTQRERQKG-LPRQVFEQDASGDERSGPEDSNDSRRGSGSP 179
hCLASP1          WLYKGNFNSTVNNTVTVRSFKKRYFQLTQLPDNSYIMNFYKDEKISKEPK-GCIFLDSCT 239
                    : :               .::      *    :  :     .  :   .    .

hCLASP4          DVVQCPKMRRHAFELKMLDKYSHYLAAETEQEMEEWLITLKKIIQINTDSLVQEKKETVE 222
hCLASP5          DVSGKGPVTACDFDLRSLQPDKRLENLLQQVSAEDFEKQNEEARRTN---------RQAE 169
hCLASP3          DDTPRGSWACSIFDLKNSLPDALLPNLLDRTPNEEIDRQNDDQRKSN---------RHKE 234
hCLASP2          GVVQNNKVRRFAFELKMQDKSSYLLAADSEVEMEEWITILNKILQLN-----FEAAMQEK 219
hCLASP7          EDTPRSSGASSIFDLRNLAADSLLPSLLERAAPEDVDRRNETLRRQH---------RPPA 230
hCLASP1          GVVQNNRLRKYAFELKMNDLTYFVLAAETESDMDEWIHTLNRILQISPEGPLQGRRSTEL 299
                            *:*:              .   ::     .   :

hCLASP4          TAQDDETSS----QGKAENIMASLERSMHPELMKYGRETEQLNKLSRGDGRQNLFSFDSE 278
hCLASP5          LFALYPSVD----EEDAVEIRPVPECPKEHLG-------N------RILVKLLTLKFEIE 212
hCLASP3          LFALHPSPD----EEEPIERLSVPDIPKEHFG-------------QRLLVKCLSLKFEIE 277
hCLASP2          RNGDSHEDD----EQSKLEGSGSGLDSYLPELAKSAREAEIK---LKSESRVKLFYLDPD 272
hCLASP7          LLTLYPAPD----EDEAVERCSRPEPPREHFG-------------QRILVKCLSLKFEIE 273
hCLASP1          TDLGLDSLDNSVTCECTPEETDSSENNLHADFAKYLTETEDTVKTTRNMERLNLFSLDPD 359
                        .        :                                :   :   : :: :

hCLASP4          VQRLDFS----GIEPDIKP-FEEKCNKRFLVNCHDLTFNILGQIGDNAKGPPTNVEPFFI 333
hCLASP5          IEPLFAS----IALYDVKERKKISENFHCDLNSDQFKGFLRAHTPSVAASSQARSAVFSV 268
hCLASP3          IEPIFAS----LALYDVKEKKKISENFYFDLNSEQMKGLLRPHVPPAAITTLARSAIFSI 333
hCLASP2          AQKLDFS----SAEPEVKS-FEEKFGKRILVKCNDLSFNLQCCVAENEEGPTTNVEPFFV 327
hCLASP7          IEPIFGI----LALYDVREKKKISENFYFDLNSDSMKGLLRAHGTHPAISTLARSAIFSV 329
hCLASP1          IDTLKLQKKDLLEPESVIKPFEEKAAKRIMIICKALNSNLQGCVTENENDPITNIEPFFV 419
                  : :           .:    : .      : .. :.  :          . :.   * :
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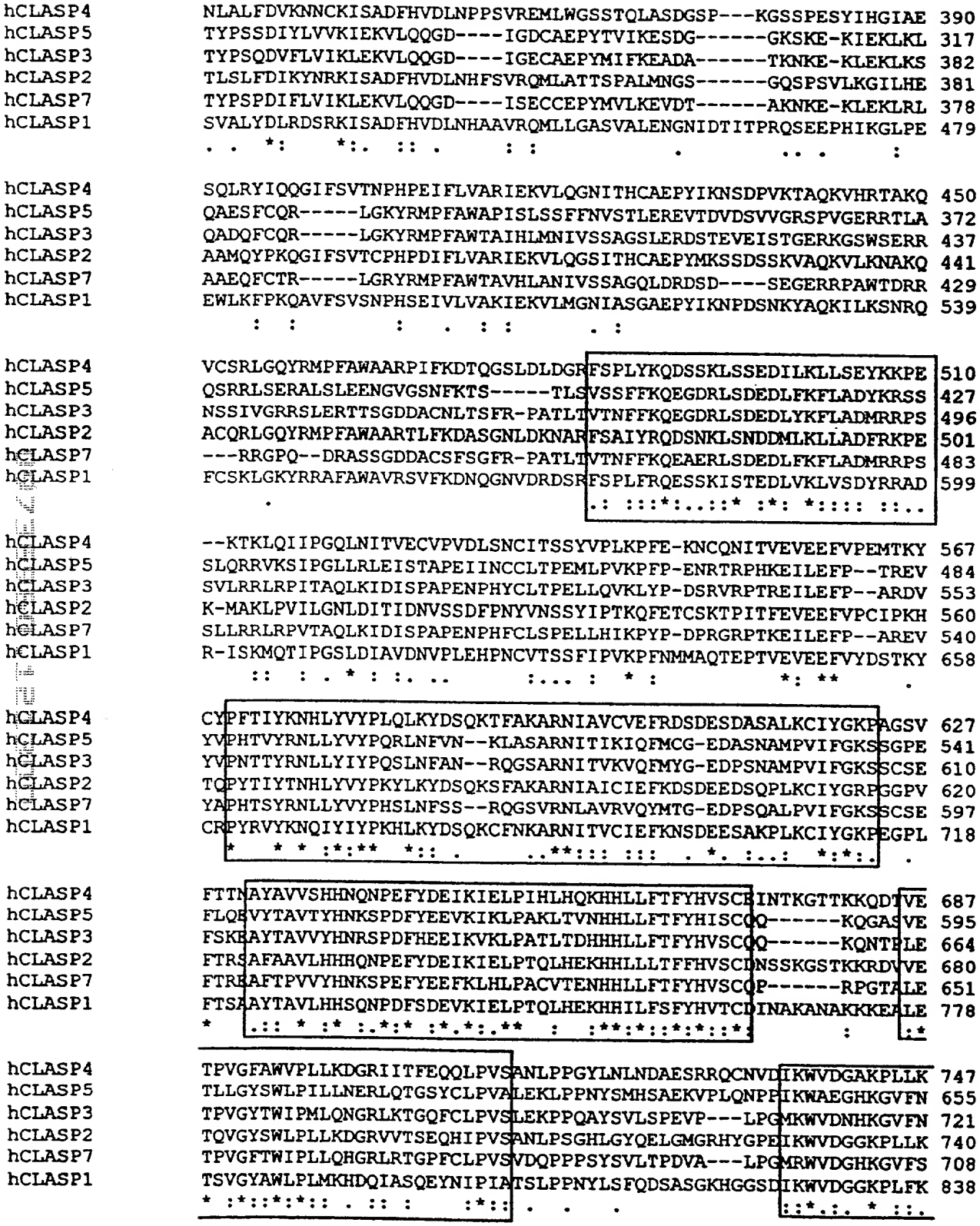
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hCLASP3 TYPSQDVFLVIKLEKVLQQGD----IGECAEPYMIFKEADA------TKNKE-KLEKLKS 382
hCLASP2 TLSLFDIKYNRKISADFHVDLNHFSVRQMLATTSPALMNGS------GQSPSVLKGILHE 381
hCLASP7 TYPSPDIFLVIKLEKVLQQGD----ISECCEPYMVLKEVDT------AKNKE-KLEKLRL 378
hCLASP1 SVALYDLRDSRKISADFHVDLNHAAVRQMLLGASVALENGNIDTITPRQSEEPHIKGLPE 479
hCLASP4 SQLRYIQQGIFSVTNPHPEIFLVARIEKVLQGNITHCAEPYIKNSDPVKTAQKVHRTAKQ 450
hCLASP5 QAESFCQR-----LGKYRMPFAWAPISLSSFFNVSTLEREVTDVDSVVGRSPVGERRTLA 372
hCLASP3 QADQFCQR-----LGKYRMPFAWTAIHLMNIVSSAGSLERDSTEVEISTGERKGSWSERR 437
hCLASP2 AAMQYPKQGIFSVTCPHPDIFLVARIEKVLQGSITHCAEPYMKSSDSSKVAQKVLKNAKQ 441
hCLASP7 AAEQFCTR-----LGRYRMPFAWTAVHLANIVSSAGQLDRDSD----SEGERRPAWTDRR 429
hCLASP1 EWLKFPKQAVFSVSNPHSEIVLVAKIEKVLMGNIASGAEPYIKNPDSNKYAQKILKSNRQ 539
hCLASP4 VCSRLGQYRMPFAWAARPIFKDTQGSLDLDGRFSPLYKQDSSKLSSEDILKLLSEYKKPE 510
hCLASP5 QSRRLSERALSLEENGVGSNFKTS-----TLSVSSFFKQEGDRLSDEDLFKFLADYKRSS 427
hCLASP3 NSSIVGRRSLERTTSGDDACNLTSFR-PATLTVTNFFKQEGDRLSDEDLYKFLADMRRPS 496
hCLASP2 ACQRLGQYRMPFAWAARTLFKDASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPE 501
hCLASP7 ---RRGPQ--DRASSGDDACSFSGFR-PATLTVTNFFKQEAERLSDEDLFKFLADMRRPS 483
hCLASP1 FCSKLGKYRRAFAWAVRSVFKDNQGNVDRDSRFSPLFRQESSKISTEDLVKLVSDYRRAD 599
hCLASP4 --KTKLQIIPGQLNITVECVPVDLSNCITSSYVPLKPFE-KNCQNITVEVEEFVPEMTKY 567
hCLASP5 SLQRRVKSIPGLLRLEISTAPEIINCCLTPEMLPVKPFP-ENRTRPHKEILEFP--TREV 484
hCLASP3 SVLRRLRPITAQLKIDISPAPENPHYCLTPELLQVKLYP-DSRVRPTREILEFP--ARDV 553
hCLASP2 K-MAKLPVILGNLDITIDNVSSDFPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKH 560
hCLASP7 SLLRRLRPVTAQLKIDISPAPENPHFCLSPELLHIKPYP-DPRGRPTKEILEFP--AREV 540
hCLASP1 R-ISKMQTIPGSLDIAVDNVPLEHPNCVTSSFIPVKPFNMMAQTEPTVEVEEFVYDSTKY 658
hCLASP4 CYPFTIYKNHLYVYPLQLKYDSQKTFAKARNIAVCVEFRDSDESDASALKCIYGKPAGSV 627
hCLASP5 YVPHTVYRNLLYVYPQRLNFVN--KLASARNITIKIQFMCG-EDASNAMPVIFGKSSGPE 541
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hCLASP2 TQPYTIYTNHLYVYPKYLKYDSQKSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPV 620
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hCLASP1 CRPYRVYKNQIYIYPKHLKYDSQKCFNKARNITVCIEFKNSDEESAKPLKCIYGKPEGPL 718
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hCLASP5 FLQSVYTAVTYHNKSPDFYEEVKIKLPAKLTVNHHLLFTFYHISCQQ------KQGASVE 595
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hCLASP3 TPVGYTWIPMLQNGRLKTGQFCLPVSLEKPPQAYSVLSPEVP---LPGMKWVDNHKGVFN 721
hCLASP2 TQVGYSWLPLLKDGRVVTSEQHIPVSANLPSGHLGYQELGMGRHYGPEIKWVDGGKPLLK 740
hCLASP7 TPVGFTWIPLLQHGRLRTGPFCLPVSVDQPPPSYSVLTPDVA---LPGMRWVDGHKGVFS 708
hCLASP1 TSVGYAWLPLMKHDQIASQEYNIPIATSLPPNYLSFQDSASGKHGGSDIKWVDGGKPLFK 838

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hCLASP4 FKSHLESTIYTQDLHVHKFFHHCQLIQS----------GSKEVPGELIKYLKCLHAM 794
hCLASP5 IEVQAVSSVHTQDNHLEKFFTLCHSLESQVTFPIRVLDQKISEMALEHELKLSIICLNSS 715
hCLASP3 VEVVAVSSIHTQDPYLDKFFALVNALDEH-LFPVRIGDMRIMENNLENELKSSISALNSS 780
hCLASP2 ISTHLVSTVYTQDQHLHNFFQYCQKTES----------GAQALGNELVKYLKSLHAM 787
hCLASP7 VELTAVSSVHPQDPYLDKFFTLVHVLEEG-AFPFRLKDTVLSEGNVEQELRASLAALRLA 767
hCLASP1 VSTFVVSTVNTQDPHVNAFFQECQKREKD----------MSQSPTSNFIRSCKNLLNVE 887
hCLASP4 EIQVMIQFLPVILMQLFR----------VLTNMTH------EDDVP 824
hCLASP5 RLEPLVLFLHLVLDKLFQLSVQPMVIAGQTANFSQFAFESVVAIANSLHNSKDLSKDQHG 775
hCLASP3 QLEPVVRFLHLLLDKLILLVIRPPVIAGQIVNLGQASFEAMASIINRLHKNLEGNHDQHG 840
hCLASP2 EGHVMIAFLPTILNQLFR----------VLT-RAT------QEEVA 816
hCLASP7 SPEPLVAFSHHVLDKLVRLVIRPPIISGQIVNLGRGAFEAMAHVVSLVHRSLEAAQDARG 827
hCLASP1 KIHAIMSFLPIILNQLFK----------VLVQNE------EDEIT 916
hCLASP4 INCTMV-LLHIVSKCHEEGLDS----------YLRSFIKYS----------FRPEKP 860
hCLASP5 RNCLLASYVHYVFRLPEVQRDVPKSGAPTALLDPRSYHTYGRTSAAAVSSKLLQARVMSS 835
hCLASP3 RNSLLASYIHYVFRLPNTYPNSSSPG-PGGLGGSVHYATMARSAVRPASLNLNRSRSLSN 899
hCLASP2 VNVTRV-IIHVVAQCHEEGLES----------HLRSYVKYA----------YKAEPY 852
hCLASP7 HCPQLAAYVHYAFRLPGTEPSLPDGAPP----VTVQAATLARGSGRPASLYLARSKSISS 883
hCLASP1 TTVTRV-LPDIVAKCHEEQLDH----------SVQSYIKFV----------FKTRAC 952
hCLASP4 SAPQAQLIH-------ETLATTMIAILKQS---------- 883
hCLASP5 SNPDLAGTHSAADEEVKNIMSSKIADRNCSRMSYYCSGSSDAPSSPA---------- 882
hCLASP3 SNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAESTQAMDRSC 959
hCLASP2 VASEYKTVH-------EELTKSMTTILKPS---------- 875
hCLASP7 SNPDLAVAPGSVDDEVSRILASKLLHEELA-LQ---------- 915
hCLASP1 KE---RPVH-------EDLAKNVTGLLKSN---------- 972
hCLASP4 ----------ADFLSINKLLKYS----------WFFFEIIAKSM 907
hCLASP5 ----------APRPASKKHFHEELALQ----------MVVSTGMVKSM 910
hCLASP3 NRMSSHTETSSFLQTLTGRLPTKKLFHEELALQWVVCSGSVRESALQQAWFFFELMVKSM 1019
hCLASP2 ----------ADFLTSNKLLRYS----------WFFFDVLIKSM 899
hCLASP7 ----------WVVSSSAVREAILQHA----------WFFFQLMVKSM 942
hCLASP1 ----------DSPTVKHVLKHS----------WFFFAIILKSM 995
Cadherin Cleavage
hCLASP4 ATYLLEENKIKLERGQRFPETYHHVLHSLLLAIIPHVTIRYAEIPDE---SRNVNYSLAS 964
hCLASP5 AQHVHNMDKRDSERRTRFSDRFMDDITTIVNVVTSEIAALLVKPQKENEQAEKMNISLAF 970
hCLASP3 VHHLYFNDKLEAERKSRFPERFMDDIAALVSTIASDIVSRFQKDTEM---VERLNTSLAF 1076
hCLASP2 AQHLIENSKVKLLRNQRFPASYHHAAETVVNMLMPHITQKFGDNPEA---SKNANHSLAV 956
hCLASP7 ALHLLLGQRLDTERKLRFPGRFLDDITALVGSVGLEVITRVHKDVEL---AEHLNASLAF 999
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hCLASP3 FLNDLLSVMDRGFVFSLIKSCYKQVSSKLYSLPNPSVLVSLRLDFLRIICSHEHYVTLNL 1136
hCLASP2 FIKRCFTFMDRGFVFKQINNYISCFAPGDP-----KTLFEYKFEFLRVVCNHEHYIPLNL 1011
hCLASP7 FLSDLLSLVDRGFVFSLVRAHYKQVATRLQSSPNPAALLTLRMEFTRILCSHEHYVTLNL 1059
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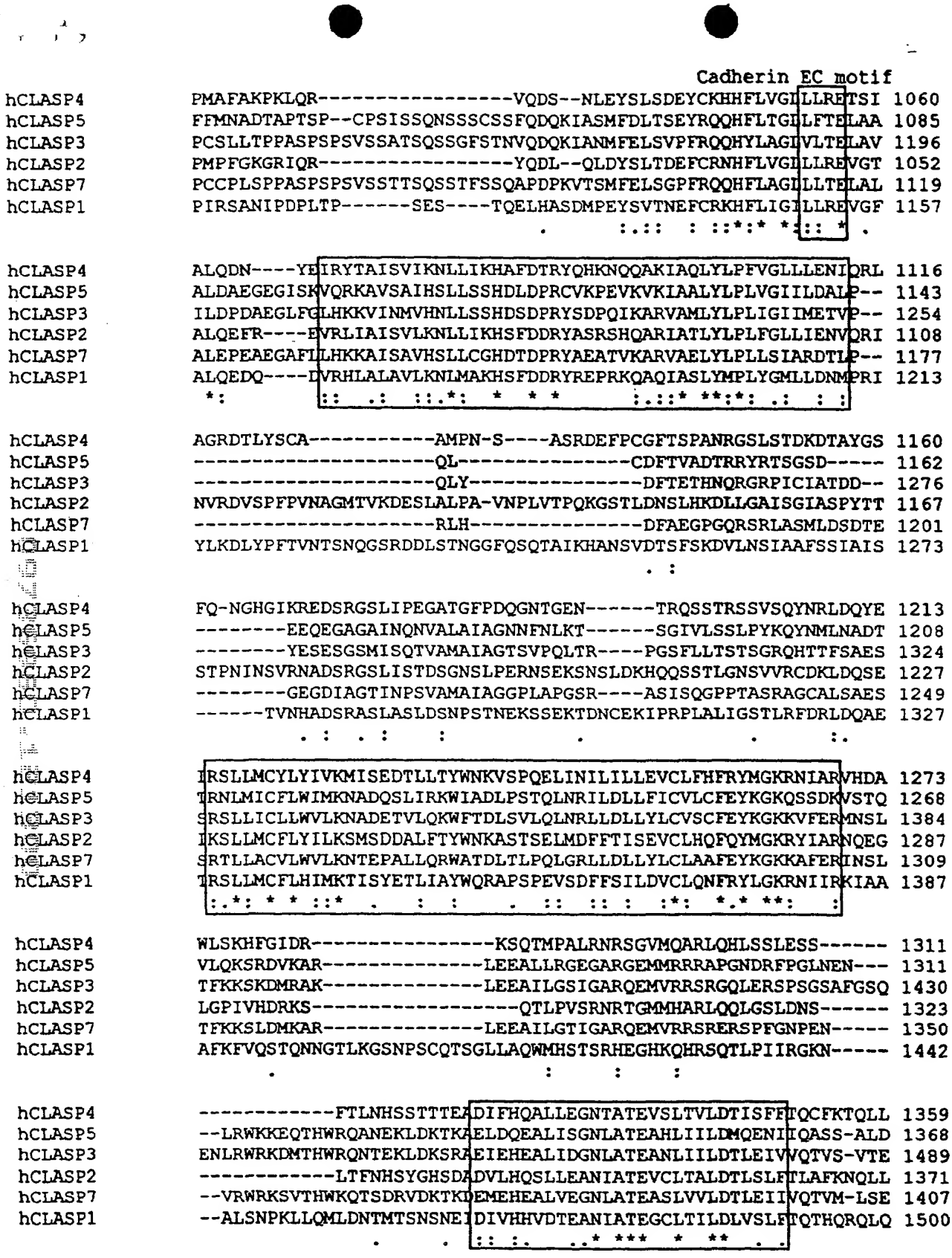
Cadherin EC motif
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hCLASP3 PCSLLTPPASPSPSVSSATSQSSGFSTNVQDQKIANMFELSVPFRQQHYLAGLVLTELAV 1196
hCLASP2 PMPFGKGRIQR----------YQDL--QLDYSLTDEFCRNHFLVGLLLREVGT 1052
hCLASP7 PCCPLSPPASPSPSVSSTTSQSSTFSSQAPDPKVTSMFELSGPFRQQHFLAGLLLTELAL 1119
hCLASP1 PIRSANIPDPLTP------SES----TQELHASDMPEYSVTNEFCRKHFLIGLLLREVGF 1157
hCLASP4 ALQDN----YEIRYTAISVIKNLLIKHAFDTRYQHKNQQAKIAQLYLPFVGLLLENIQRL 1116
hCLASP5 ALDAEGEGISKVQRKAVSAIHSLLSSHDLDPRCVKPEVKVKIAALYLPLVGIILDALP-- 1143
hCLASP3 ILDPDAEGLFGLHKKVINMVHNLLSSHDSDPRYSDPQIKARVAMLYLPLIGIIMETVP-- 1254
hCLASP2 ALQEFR----EVRLIAISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRI 1108
hCLASP7 ALEPEAEGAFLLHKKAISAVHSLLCGHDTDPRYAEATVKARVAELYLPLLSIARDTLP-- 1177
hCLASP1 ALQEDQ----DVRHLALAVLKNLMAKHSFDDRYREPRKQAQIASLYMPLYGMLLDNMPRI 1213
hCLASP4 AGRDTLYSCA----------AMPN-S----ASRDEFPCGFTSPANRGSLSTDKDTAYGS 1160
hCLASP5 ----------QL----------CDFTVADTRRYRTSGSD----- 1162
hCLASP3 ----------QLY----------DFTETHNQRGRPICIATDD-- 1276
hCLASP2 NVRDVSPFPVNAGMTVKDESLALPA-VNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTT 1167
hCLASP7 ----------RLH----------DFAEGPGQRSRLASMLDSDTE 1201
hCLASP1 YLKDLYPFTVNTSNQGSRDDLSTNGGFQSQTAIKHANSVDTSFSKDVLNSIAAFSSIAIS 1273
hCLASP4 FQ-NGHGIKREDSRGSLIPEGATGFPDQGNTGEN------TRQSSTRSSVSQYNRLDQYE 1213
hCLASP5 --------EEQEGAGAINQNVALAIAGNNFNLKT------SGIVLSSLPYKQYNMLNADT 1208
hCLASP3 --------YESESGSMISQTVAMAIAGTSVPQLTR----PGSFLLTSTSGRQHTTFSAES 1324
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hCLASP7 --------GEGDIAGTINPSVAMAIAGGPLAPGSR----ASISQGPPTASRAGCALSAES 1249
hCLASP1 ------TVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPLALIGSTLRFDRLDQAE 1327
hCLASP4 IRSLLMCYLYIVKMISEDTLLTYWNKVSPQELINILILLEVCLFHFRYMGKRNIARVHDA 1273
hCLASP5 TRNLMICFLWIMKNADQSLIRKWIADLPSTQLNRILDLLFICVLCFEYKGKQSSDKVSTQ 1268
hCLASP3 SRSLLICLLWVLKNADETVLQKWFTDLSVLQLNRLLDLLYLCVSCFEYKGKKVFERMNSL 1384
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hCLASP1 TRSLLMCFLHIMKTISYETLIAYWQRAPSPEVSDFFSILDVCLQNFRYLGKRNIIRKIAA 1387
hCLASP4 WLSKHFGIDR----------KSQTMPALRNRSGVMQARLQHLSSLESS------ 1311
hCLASP5 VLQKSRDVKAR----------LEEALLRGEGARGEMMRRRAPGNDRFPGLNEN--- 1311
hCLASP3 TFKKSKDMRAK----------LEEAILGSIGARQEMVRRSRGQLERSPSGSAFGSQ 1430
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hCLASP7 TFKKSLDMKAR----------LEEAILGTIGARQEMVRRSRERSPFGNPEN----- 1350
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hCLASP4 ----------FTLNHSSTTTEADIFHQALLEGNTATEVSLTVLDTISFFTQCFKTQLL 1359
hCLASP5 --LRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAHLIILDMQENIIQASS-ALD 1368
hCLASP3 ENLRWRKDMTHWRQNTEKLDKSRAEIEHEALIDGNLATEANLIILDTLEIVWQTVS-VTE 1489
hCLASP2 ----------LTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFTLAFKNQLL 1371
hCLASP7 --VRWRKSVTHWKQTSDRVDKTKDEMEHEALVEGNLATEASLVVLDTLEIIWQTVM-LSE 1407
hCLASP1 --ALSNPKLLQMLDNTMTSNSNEIDIVHHVDTEANIATEGCLTILDLVSLFTQTHQRQLQ 1500

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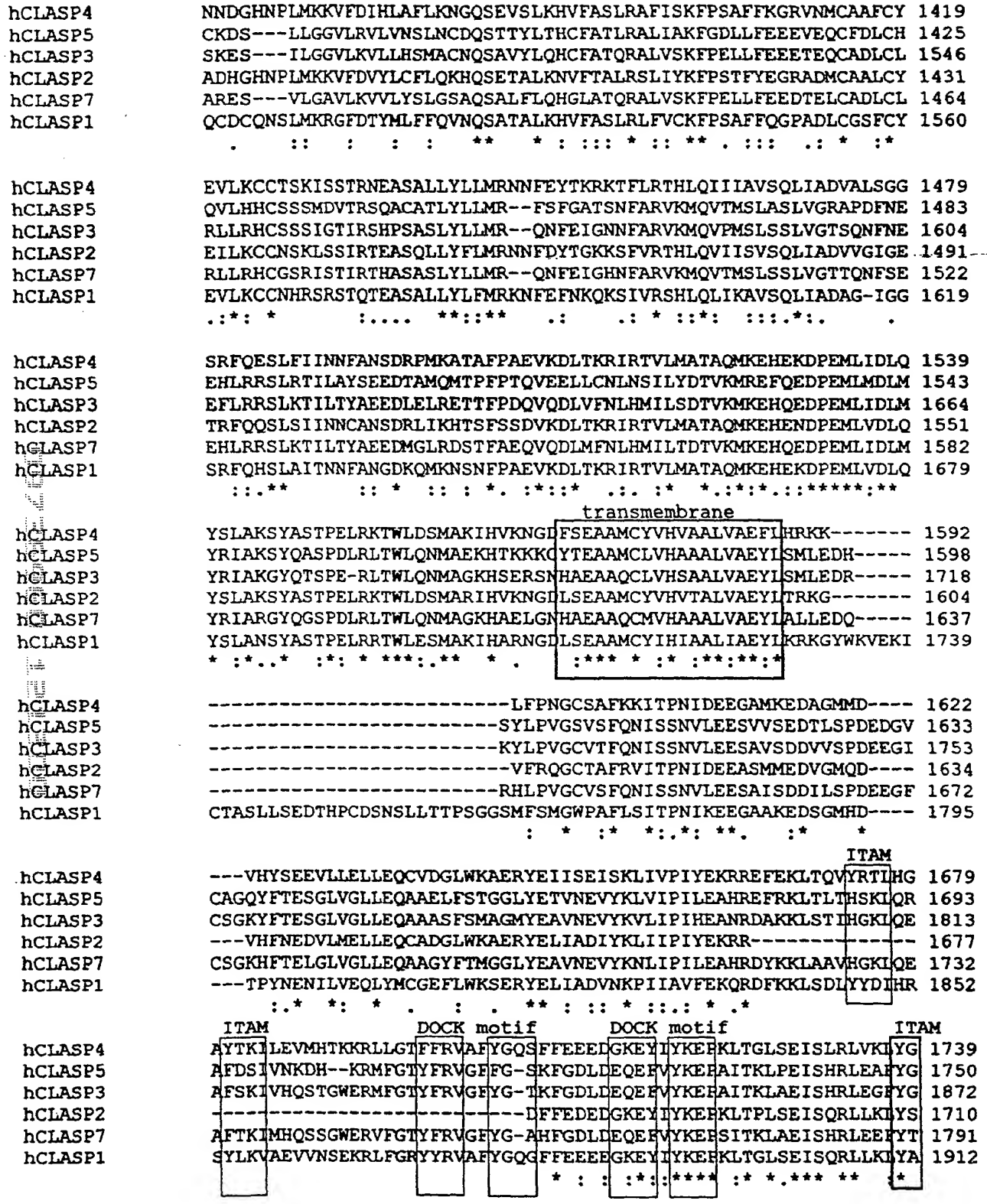
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hCLASP3 SKES---ILGGVLKVLLHSMACNQSAVYLQHCFATQRALVSKFPELLFEEETEQCADLCL 1546
hCLASP2 ADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRADMCAALCY 1431
hCLASP7 ARES---VLGAVLKVVLYSLGSAQSALFLQHGLATQRALVSKFPELLFEEDTELCADLCL 1464
hCLASP1 QCDCQNSLMKRGFDTYMLFFQVNQSATALKHVFASLRLFVCKFPSAFFQGPADLCGSFCY 1560
hCLASP4 EVLKCCTSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTHLQIIIAVSQLIADVALSGG 1479
hCLASP5 QVLHHCSSSMDVTRSQACATLYLLMR--FSFGATSNFARVKMQVTMSLASLVGRAPDFNE 1483
hCLASP3 RLLRHCSSSIGTIRSHPSASLYLLMR--QNFEIGNNFARVKMQVPMSLSSLVGTSQNFNE 1604
hCLASP2 EILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKSFVRTHLQVIISVSQLIADVVGIGE 1491
hCLASP7 RLLRHCGSRISTIRTHASASLYLLMR--QNFEIGHNFARVKMQVTMSLSSLVGTTQNFSE 1522
hCLASP1 EVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSHLQLIKAVSQLIADAG-IGG 1619
hCLASP4 SRFQESLFIINNFANSDRPMKATAFPAEVKDLTKRIRTVLMATAQMKEHEKDPEMLIDLQ 1539
hCLASP5 EHLRRSLRTILAYSEEDTAMQMTPFPTQVEELLCNLNSILYDTVKMREFQEDPEMLMDLM 1543
hCLASP3 EFLRRSLKTILTYAEEDLELRETTFPDQVQDLVFNLHMILSDTVKMKEHQEDPEMLIDLM 1664
hCLASP2 TRFQQSLSIINNCANSDRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHENDPEMLVDLQ 1551
hCLASP7 EHLRRSLKTILTYAEEDMGLRDSTFAEQVQDLMFNLHMILTDTVKMKEHQEDPEMLIDLM 1582
hCLASP1 SRFQHSLAITNNFANGDKQMKNSNFPAEVKDLTKRIRTVLMATAQMKEHEKDPEMLVDLQ 1679
transmembrane
hCLASP4 YSLAKSYASTPELRKTWLDSMAKIHVKNGDFSEAAMCYVHVAALVAEFLHRKK------- 1592
hCLASP5 YRIAKSYQASPDLRLTWLQNMAEKHTKKKQYTEAAMCLVHAAALVAEYLSMLEDK------ 1598
hCLASP3 YRIAKGYQTSPE-RLTWLQNMAGKHSERSNHAEAAQCLVHSAALVAEYLSMLEDR------ 1718
hCLASP2 YSLAKSYASTPELRKTWLDSMARIHVKNGDLSEAAMCYVHVTALVAEYLTRKG------- 1604
hCLASP7 YRIARGYQGSPDLRLTWLQNMAGKHAELGNHAEAAQCMVHAAALVAEYLALLEDQ------ 1637
hCLASP1 YSLANSYASTPELRRTWLESMAKIHARNGDLSEAAMCYIHIAALIAEYLKRKGYWKVEKI 1739
hCLASP4 ----------LFPNGCSAFKKITPNIDEEGAMKEDAGMMD---- 1622
hCLASP5 ----------SYLPVGSVSFQNISSNVLEESVVSEDTLSPDEDGV 1633
hCLASP3 ----------KYLPVGCVTFQNISSNVLEESAVSDDVVSPDEEGI 1753
hCLASP2 ----------VFRQGCTAFRVITPNIDEEASMMEDVGMQD---- 1634
hCLASP7 ----------RHLPVGCVSFQNISSNVLEESAISDDILSPDEEGF 1672
hCLASP1 CTASLLSEDTHPCDSNSLLTTPSGGSMFSMGWPAFLSITPNIKEEGAAKEDSGMHD---- 1795
ITAM
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hCLASP3 CSGKYFTESGLVGLLEQAAASFSMAGMYEAVNEVYKVLIPIHEANRDAKKLSTIHGKLQE 1813
hCLASP2 ---VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIIPIYEKRR---------- 1677
hCLASP7 CSGKHFTELGLVGLLEQAAGYFTMGGLYEAVNEVYKNLIPILEAHRDYKKLAAVHGKLQE 1732
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ITAM DOCK motif DOCK motif ITAM
hCLASP4 AYTKILEVMHTKKRLLGTFFRVAFYGQSFFEEELGKEYIYKEFKLTGLSEISLRLVKLYG 1739
hCLASP5 AFDSIVNKDH--KRMFGTYFRVGFFG-SKFGDLDEQEFVYKEFAITKLPEISHRLEAFYG 1750
hCLASP3 AFSKIVHQSTGWERMFGTYFRVGFYG-TKFGDLDEQEFVYKEFAITKLAEISHRLEGFYG 1872
hCLASP2 ----------DFFEDELGKEYIYKEFKLTPLSEISQRLLKLYS 1710
hCLASP7 AFTKIMHQSSGWERVFGTYFRVGFYG-AHFGDLDEQEFVYKEFSITKLAEISHRLEEFYT 1791
hCLASP1 SYLKVAEVVNSEKRLFGRYYRVAFYGQGFFEEEEGKEYIYKEFKLTGLSEISQRLLKLYA 1912

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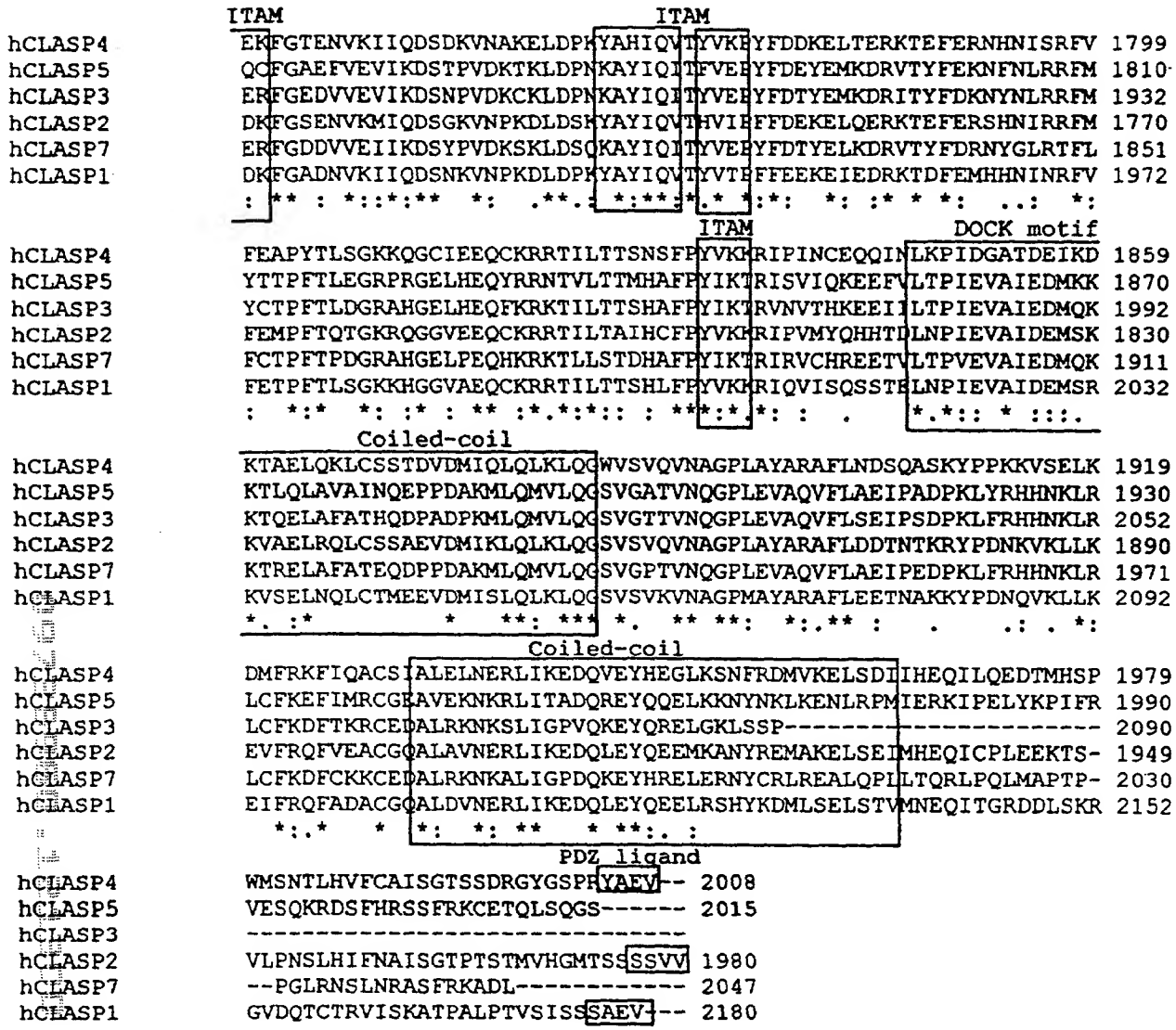
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ITAM
ITAM
DOCK motif
Coiled-coil
Coiled-coil
PDZ ligand
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hCLASP7
hCLASP1

FIG. 8
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